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RA Raha S.S., Loquellano N.A., McKernan K.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hate S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N; TISSUE=Mammary tumor. Metallothionien-TGF alpha model.
RC 10 month old virgin mouse. Taken by biopsy.;
RG NIH MGC Project;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL: BC051033; AH51033.1; -; mRNA.
DR Ensembl: ENSMUSG0000057092; Mus musculus.
DR MGI: MGI:107497; Fxyd3.
DR GO: GO:0005615; C:extracellular space; RCA.
DR GO: GO:0016021; C:integral to membrane; RCA.
DR InterPro: IPR000272; FXYD.
DR Pfam: PF02038; ATP1G1_PLM MAT8; 1.
DR PROSITE: PS01310; FXYD; 1.
SQ SEQUENCE 70 AA; 7773 MW; AB2A5EAF1490BF08 CRC64;

Query Match 44.0%; Score 203; DB 2; Length 70;
Best Local Similarity 59.4%; Pred. No. 8e-14;
Matches 41; Conservative 10; Mismatches 16; Indels 2; Gaps 2;

QY 1 MERVTLALL-LLAGLTALANDPFANKDDPFYDWNQLQSLGICGGLLAIAAGIAVLGSK 59
DB 1 MQEVLISLLVLLAGLTALDNDP-ENKNDPFYDWSLRVGGICAGILCALGIIIVMSG 59

QY 60 KCKYKSSQK 68
DB 60 KCKKCFRQK 68

RESULT 13
ID Q3SZX0_BOVIN PRELIMINARY; PRT; 92 AA.
AC Q3SZX0;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-MAR-2006, entry version 4.
DE Hypothetical protein.
OS Bos taurus [Bovine].
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Crossbred x Angus; TISSUE=Liver;
RA Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shermen C.,
RA Wagner L., Balu M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
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DR EMBL: BC102671; AAI02672.1; -; mRNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005216; F:ion channel activity; IEA.
DR GO: GO:0006811; F:ion transport; IEA.
DR InterPro: IPR000272; FXYD.
DR Pfam: PF02038; ATP1G1_PLM MAT8; 1.
DR PROSITE: PS01310; FXYD; 1.
KW Hypothetical protein.
SQ SEQUENCE 92 AA; 10447 MW; 42244DD050C60A3B CRC64;

Query Match 28.5%; Score 131.5; DB 2; Length 92;
Best Local Similarity 38.2%; Pred. No. 4.8e-06;
Matches 29; Conservative 18; Mismatches 28; Indels 1; Gaps 1;

QY 1 MERVTLALLLLAGLTALANDPFANKDDPFYDWNQLQSLGICGGLLAIAAGIAVLGSK 60
DB 1 MASLSHILVLCVGLLAM-VNAEAPQEHDPFTYDQSLRGIIAGILFILGILVLSRR 59

QY 61 CKYKSSQKOHSPVPEK 76
DB 60 CRCKFNQQRTEGPDE 75

RESULT 14
ID_PLM_HUMAN STANDARD; PRT; 92 AA.
AC O00168;
DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT 30-AUG-2002, sequence version 2.
DT 07-FEB-2006, entry version 47.
DE Phospholemmann precursor (FXYD domain-containing ion transport
DE regulator 1).
GN Name=FXYD1; Synonyms=PLM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Heart;
RC MEDLINE=97312702; PubMed=9169143; DOI=10.1006/geno.1997.4665;
RA Chen L.-S.K., Lo C.F., Numann R., Cuddy M.;
RA "Characterization of the human and rat phospholemmann (PLM) cDNAs and
RA localization of the human PLM gene to chromosome 19q13.1.";
RL Genomics 41:435-443(1997).
[2]
RN NUCLEOTIDE SEQUENCE [MRNA].
RP MEDLINE=20408885; PubMed=10950925; DOI=10.1006/geno.2000.6274;
RA Sweadner K.J., Rael E.;
RA "The FXYD gene family of small ion transport regulators or channels:
RA cDNA sequence, protein signature sequence, and expression.";
RL Genomics 68:41-56(2000).
[3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP TISSUE=Brain, Lung, and Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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DR PROSITE: PS01310; FXVD: 1.
KW Chloride; Chloride channel; Ion transport; Ionic channel; Membrane;
KW Signal; Transmembrane; Transport.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 87
FT
FT FXVD domain-containing ion transport
FT regulator 3.
FT /FTID=PRO 0000010362.
FT TOPO DOM 21 38 Extracellular (Potential).
FT TRANSMEM 39 59 Potential.
FT TOPO DOM 60 87 Cytoplasmic (Potential).
FT CONFLICT 36 37 Missing (in Ref. 2).
FT CONFLICT 58 58 S -> SEWRSSGEQGRGWGSPPLTLTQLSPGTG (in Ref. 2).
FT
SQ SEQUENCE 87 AA; 9263 MW; 6D674D668EB32493 CRC64;

Query Match 46.5%; Score 214.5; DB 1; Length 87;
Best Local Similarity 54.5%; Pred. No. 5.9e-15;
Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;

QY 1 MERVTLALL-LAGLTALANDPPFANKDDPPYDWNKQLSLGICGGLAAGIAGIIVLSG 59
Db 1 MOKVTGLLVLAGFPVLDAND-LEDKNSPFYDWHSLQVGLICAGVLCAMGIIVMSA 59
QY 60 KCKYSSQKQ-HSPVPEKAIPITPGSA 86
Db 60 KCKKFGQSGHH--PGTPTPLITPGSA 85

RESULT 11
Q61B59 HUMAN
ID Q61B59 HUMAN PRELIMINARY; PRT; 87 AA.
AC Q61B59
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE FXVD3 protein (FXVD domain containing ion transport regulator 3, isoform 1).
GN Name=FXVD3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Mfoundinya M., Schick M., Eisenstein S., Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W., Korn B., Zuo D., Hu Y., LaBaer J.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., Phelan M., Farmer A.;
RA "Cloning of human full-length CDSS in BD Creator(TM) System Donor vector";
RA Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=White Matter pool- 5 brain tissues- femoral artery;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stachenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=White Matter pool- 5 brain tissues- femoral artery;
RA Director MGC Project;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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CC
EMBL; CR456945; CAG33226.1; -; mRNA.
DR EMBL; CR542197; CAG46994.1; -; mRNA.
DR EMBL; BT006712; AAP35358.1; -; mRNA.
DR EMBL; BC090044; AAH90044.1; -; mRNA.
DR Ensembl; ENSG0000089356; Homo sapiens.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR00272; FXVD.
DR Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR PROSITE; PS01310; FXVD; 1.
SQ SEQUENCE 87 AA; 9263 MW; 6D674D668EB32493 CRC64;

Query Match 46.5%; Score 214.5; DB 2; Length 87;
Best Local Similarity 54.5%; Pred. No. 5.9e-15;
Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;

QY 1 MERVTLALL-LAGLTALANDPPFANKDDPPYDWNKQLSLGICGGLAAGIAGIIVLSG 59
Db 1 MOKVTGLLVLAGFPVLDAND-LEDKNSPFYDWHSLQVGLICAGVLCAMGIIVMSA 59
QY 60 KCKYSSQKQ-HSPVPEKAIPITPGSA 86
Db 60 KCKKFGQSGHH--PGTPTPLITPGSA 85

RESULT 12
Q80UV3 MOUSE
ID Q80UV3_MOUSE PRELIMINARY; PRT; 70 AA.
AC Q80UV3;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Fxyd3 protein.
GN Name=Fxyd3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. Metallothionien-TGF alpha model.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stachenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,

Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DE	FXD domain-containing ion transport regulator 3 precursor (Chloride conductance inducer protein Mat-8) (Mammary tumor 8 kDa protein)
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DE	(Phospholemman-like).
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	GN	Name=FXD3; Synonyms=MAT8, PMLL;
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	OS	Homo sapiens (Human)
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	OC	Homo
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	OX	NCBI_TaxID=9606;
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	OX	[1]
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RN	NUCLEOTIDE SEQUENCE [MRNA]
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RP	TISSUE=Mammary gland;
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RC	MEDLINE=95138184; PubMed=7836447; DOI=10.1074/jbc.270.15.8571;
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RX	Morrison B.W., Moorman J.R., Kowdley G.C., Kobayashi Y.M., Jones L.R.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Leder P.;
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	"Mat-8, a novel phospholemman-like protein expressed in human breast
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RT	tumors, induces a chloride conductance in Xenopus oocytes.";
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RT	J. Biol. Chem. 270:2176-2182(1995).
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RT	[2]
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RN	NUCLEOTIDE SEQUENCE [MRNA]
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RP	TISSUE=Lung carcinoma;
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RC	Lei W., Wu M.;
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RL	[3]
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RN	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RP	TISSUE=Urinary bladder;
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Bosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Richards S., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RT	"Generation and initial analysis of more than 15,000 full-length human
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RT	and mouse cDNA sequences.";
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	CC	-!- FUNCTION: Induces a hyperpolarization-activated chloride current
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	CC	when expressed in Xenopus oocytes. May be a modulator capable of
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	CC	activating endogenous oocyte channels.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	CC	-!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	CC	protein (Potential).
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	CC	-!- TISSUE SPECIFICITY: Expressed in a subset of human breast tumors.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	CC	-!- MISCELLANEOUS: Marker of a cell type preferentially transformed by
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	CC	neu or ras oncoprotein.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	CC	-!- SIMILARITY: Belongs to the FXD family.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	CC	-----
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	CC	Distributed under the Creative Commons Attribution-NoDerivs License
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	CC	-----
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	CC	EMBL; X93036; CAA63604.1; -; mRNA.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	EMBL; U28249; AAA73922.1; -; mRNA.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	EMBL; BC005238; AA005238.1; -; mRNA.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	PIR; A55571; A55571.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	Ensembl; ENSG00000089356; Homo sapiens.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	H-InvDB; HIX0018290; -.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	HGNC; HGNC:4027; FXD3.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	MIM; 604996; gene.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	GO; GO:0005887; C:integral to plasma membrane; TAS.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	GO; GO:0005254; F:chloride channel activity; TAS.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	GO; GO:0006821; P:chloride transport; TAS.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	InterPro; IPR000272; FXD.
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
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Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	Best Local Similarity
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	Matches
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	52; Conservative
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Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	25; Indels
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Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	Best Local Similarity
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	Matches
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Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	10; Mismatches
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	25; Indels
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	3; Gaps
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Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	52; Conservative
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	10; Mismatches
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Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	52; Conservative
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	10; Mismatches
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	25; Indels
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Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	Matches
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	52; Conservative
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Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	10; Mismatches
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	25; Indels
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	3; Gaps
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Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	Query Match
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Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	10; Mismatches
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Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	Matches
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Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	10; Mismatches
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	25; Indels
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Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	Query Match
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Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	Matches
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	52; Conservative
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	10; Mismatches
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	25; Indels
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	3; Gaps
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Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	Matches
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	52; Conservative
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	10; Mismatches
Db	60	KCKCKFSQKP-SHRPGDGPPLITPGSAHNC	88	DR	25; Indels
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 DB 1 MERVTLALLAGLTALEANDPFANKDPFYDWNKQLSGLCGLLAIAAGIAVLGSK 60
 QY 61 CKYKSSQKQHSVPVPEKAIPITPGSATTC 89
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 ID FXVD4 MOUSE STANDARD; PRT; 88 AA.
 AC Q9D2W0;
 DT 23-JAN-2002, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 28.
 DE FXVD domain-containing ion transport regulator 4 precursor (Channel-
 DE inducing factor) (CHIF).
 GN Name=FXVD4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
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 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SvJ;
 RA Garty H.;
 RL "Genomic sequence of mouse CHIF (FXVD4).";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX PubMed=1641072; DOI=10.1126/science.11112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aldins V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Belsel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhury V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.B., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Green R.E.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelson J., Kitamura H.,
 RA Kitano H., Kollias A., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sanderlin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.B., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Roki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh T., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayaehizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).

RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Kidney;
 RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein (Potential).
 CC -!- SIMILARITY: Belongs to the FXVD family.
 CC
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 CC
 CC EMBL: AF362729; AAKS1508.1; -; Genomic DNA.
 CC EMBL: AK038728; BAB31372.1; -; mRNA.
 CC EMBL: BC086918; AAB86918.1; -; mRNA.
 CC Ensembl: ENSMUSG0000004988; Mus musculus.
 CC MGI: MGI:1889005; Fxyd4.
 CC GO: GO:0005615; C:extracellular space; TAS.
 CC GO: GO:0016021; C:integral to membrane; TAS.
 CC InterPro: IPR000272; FXVD.
 CC Pfam: PF02038; ATP1G_PLM_MAT8; 1.
 CC PROSITE: PS01310; FXYD; 1.
 KW Ion transport; Ionic channel; Membrane; Signal; Transmembrane;
 KW Transport.
 FT SIGNAL: 1 20 Potential
 FT CHAIN: 21 88 FXVD domain-containing ion transport
 FT regulator 4.
 FT /FTID=PRO_0000010367.
 FT TOPO_DOM: 21 38 Extracellular (Potential).
 FT TRANSMEM: 39 59 Potential.
 FT TOPO_DOM: 60 88 Cytoplasmic (Potential).
 FT SEQUENCE: 88 AA; 9269 MW; 7B0140941CFE926 CRC64;
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 Best Local Similarity 66.7%; Pred. No. 1.4e-21;
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 DB 1 MBEETCAFLLLAGLPALEASDP-VKDSPFYDWNKQLSGLCGLLAIAAGIAVLG 59
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 DB 60 KCKCRTRHP-SLPGKATPLIPGSANTC 88
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 ID FXVD4 RAT STANDARD; PRT; 87 AA.
 AC Q63113;
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 DT 01-NOV-1996, sequence version 1.
 DT 07-FEB-2006, entry version 39.
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DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
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GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20408885; PubMed=10950925; DOI=10.1006/geno.2000.6274;
RA Sweadner K.J., Rael E.;
RT "The FXD gene family of small ion transport regulators or channels:
RT cDNA sequence, protein signature sequence, and expression.";
RL Genomics 68:41-56(2000).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein (Potential).
CC -!- SIMILARITY: Belongs to the FXD family.
CC
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CC EMBL; AI829935; -; NOT ANNOTATED CDS; mRNA.
CC Ensembl; ENSG00000150201; Homo sapiens.
CC HGNC; HGNC:4028; FXD4.
CC InterPro; IPR0000272; FXD.
CC Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
CC PROSITE; PS01310; FXD; 1.
KW Ion transport; Ionic channel; Membrane; Signal; Transmembrane;
KW Transport.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 89 FXD domain-containing ion transport
FT regulator 4.
FT /FTid=PRO_0000010366.
FT TOPO_DOM 21 38 Extracellular (Potential).
FT TRANSMEM 39 59 Potential.
FT TOPO_DOM 60 89 Cytoplasmic (Potential).
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Query Match 97.6%; Score 450; DB 1; Length 89;
Best Local Similarity 97.8%; Pred. No. 3.6e-40;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 3
FXD4 HUMAN
ID FXD4 HUMAN STANDARD; PRT; 89 AA.
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DT 30-APR-2003, integrated into UniProtKB/Swiss-Prot.
DT 30-APR-2003, sequence version 1.
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OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20408885; PubMed=10950925; DOI=10.1006/geno.2000.6274;
RA Sweadner K.J., Rael E.;
RT "The FXD gene family of small ion transport regulators or channels:
RT cDNA sequence, protein signature sequence, and expression.";
RL Genomics 68:41-56(2000).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein (Potential).
CC -!- SIMILARITY: Belongs to the FXD family.
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CC
CC EMBL; AI829935; -; NOT ANNOTATED CDS; mRNA.
CC Ensembl; ENSG00000150201; Homo sapiens.
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CC InterPro; IPR0000272; FXD.
CC Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
CC PROSITE; PS01310; FXD; 1.
KW Ion transport; Ionic channel; Membrane; Signal; Transmembrane;
KW Transport.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 89 FXD domain-containing ion transport
FT regulator 4.
FT /FTid=PRO_0000010366.
FT TOPO_DOM 21 38 Extracellular (Potential).
FT TRANSMEM 39 59 Potential.
FT TOPO_DOM 60 89 Cytoplasmic (Potential).
FT SEQUENCE 89 AA; 9373 MW; B595EF99A494984 CRC64;
Query Match 97.6%; Score 450; DB 1; Length 89;
Best Local Similarity 97.8%; Pred. No. 3.6e-40;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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1419	56.5	12.3	567	2	Q4KI08_PSEF5	Q4ki08 pseudomonas
1420	56.5	12.3	570	2	Q4WD85_ASPFU	Q4wd85 aspergillus
1421	56.5	12.3	577	2	Q8SQS0_9INSE	Q8sqso tricholepid
1422	56.5	12.3	580	2	Q3HIY1_TRIER	Q3hiy1 trichodesmi
1423	56.5	12.3	589	2	Q2WSX0_CLOBE	Q2wsx0 clostridium
1424	56.5	12.3	595	1	S13A1_HUMAN	Q9bw22 homo sapien
1425	56.5	12.3	608	2	Q9BAR2_9MAGN	Q9ba20 notobuxus n
1426	56.5	12.3	611	2	Q3AEG0_CABZH	Q3aeg0 carboxydoth
1427	56.5	12.3	614	2	Q31615_BACSU	Q31615 bacillus su
1428	56.5	12.3	624	2	Q69Z90_MOUSE	Q69z90 mus musculus
1429	56.5	12.3	648	2	Q5FUH5_GLUOX	Q5fuh5 gluconobact
1430	56.5	12.3	666	2	Q4COA1_CROST	Q4coa1 crocospaer
1431	56.5	12.3	670	2	Q32212_BACSU	Q32212 bacillus su
1432	56.5	12.3	681	2	Q9BAQ3_9MAGN	Q9baq3 notobuxus a
1433	56.5	12.3	683	2	Q5CV27_CRYPV	Q5cv27 cryptospori
1434	56.5	12.3	688	2	Q9BAS3_9MAGN	Q9bas3 buxus micro
1435	56.5	12.3	686	1	VGLH_PRVKA	P27416 pseudorabie
1436	56.5	12.3	686	1	VGLH_PRVN3	P27593 pseudorabie
1437	56.5	12.3	686	1	VGLH_PRVRI	Q5ppa2 suid herpes
1438	56.5	12.3	686	2	Q5PPA2_9ALPH	Q9bas8 buxus henry
1439	56.5	12.3	688	2	Q9BAS8_9MAGN	Q7q3n1 anophelies g
1440	56.5	12.3	689	2	Q7Q3N1_ANOGA	Q9bas4 buxus ripar
1441	56.5	12.3	690	2	Q9BAS4_9MAGN	Q9bas2 buxus hilde
1442	56.5	12.3	690	2	Q9BAS2_9MAGN	Q9baq8 buxus sempe
1443	56.5	12.3	691	2	Q9BAQ8_BUXSE	Q9baq9 buxus liuki
1444	56.5	12.3	692	2	Q9BAQ9_9MAGN	Q9ba85 buxus balea
1445	56.5	12.3	692	2	Q9BAS5_9MAGN	Q9ba85 buxus micro
1446	56.5	12.3	692	2	Q9BAS5_9MAGN	Q9ba80 buxus gonoc
1447	56.5	12.3	692	2	Q9BAS7_9MAGN	Q9ba87 buxus harla
1448	56.5	12.3	695	2	Q9BAS7_9MAGN	Q9ba87 buxus harla
1449	56.5	12.3	699	2	Q9BSW4_HUMAN	Q96sw4 homo sapien
1450	56.5	12.3	704	2	Q9SC14_BUXSE	Q9sc14 buxus sempe
1451	56.5	12.3	707	2	Q9BAS6_9MAGN	Q9bas6 buxus macow
1452	56.5	12.3	710	2	Q6CGN0_YARLI	Q6cgn0 yarrowia li
1453	56.5	12.3	721	2	Q3KK27_PSRPF	Q3kk27 pseudomonas
1454	56.5	12.3	726	2	Q8HTM7_PODPE	Q8htm7 podophyllum
1455	56.5	12.3	726	2	Q8HTM9_9MAGN	Q8htm9 sinopodophy
1456	56.5	12.3	726	2	Q364T9_SHEWALL	Q364t9 shewanella
1457	56.5	12.3	729	2	Q5PXK6_RAT	Q5pxk6 rattus norv
1458	56.5	12.3	730	2	Q5PXK5_RAT	Q5pxk5 rattus norv
1459	56.5	12.3	757	1	KNCN3_HUMAN	Q14003 homo sapien
1460	56.5	12.3	758	2	Q811T2_RAT	Q811t2 rattus norv
1461	56.5	12.3	759	2	Q8HXV1_RABIT	Q8hvx1 oryctolagus
1462	56.5	12.3	769	2	Q811T3_RAT	Q811t3 rattus norv
1463	56.5	12.3	783	2	Q5NXT1_AZOSE	Q5nxt1 azoarcus sp
1464	56.5	12.3	809	2	Q2LQ19_9DELT	Q2lq19 syntrophus
1465	56.5	12.3	852	1	YKM1_YEAST	P32330 saccharomyc
1466	56.5	12.3	856	2	Q3KJ08_PSRPF	Q3kjd8 pseudomonas
1467	56.5	12.3	856	2	Q6G429_BARHE	Q6g429 bartonella
1468	56.5	12.3	889	1	KNCN3_RAT	Q01956 rattus norv
1469	56.5	12.3	894	2	Q5CGN7_CRYHO	Q5cgn7 cryptospori
1470	56.5	12.3	918	2	Q4DX98_TRYCR	Q4dx98 trypanosoma
1471	56.5	12.3	933	2	Q83GL1_TROWT	Q83gl1 tropheryma
1472	56.5	12.3	939	2	Q83HL6_TROW8	Q83hl6 tropheryma
1473	56.5	12.3	1000	2	Q5U635_HUMAN	Q5u635 homo sapien
1474	56.5	12.3	1009	2	Q5Q208_IDILO	Q5q208 idiomarina
1475	56.5	12.3	1023	2	Q43X28_SOLIBAC	Q43x28 solibacter
1476	56.5	12.3	1030	1	SEMG6_HUMAN	Q9h2e6 homo sapien
1477	56.5	12.3	1044	2	Q4CTU4_TRYCR	Q4ctu4 trypanosoma
1478	56.5	12.3	1058	2	Q5P5T6_AZOSE	Q5p5t6 azoarcus sp
1479	56.5	12.3	1127	2	Q4YF05_PLABE	Q4yf05 plasmodium
1480	56.5	12.3	1241	2	Q60RT2_CABER	Q60rt2 caenorhabdi
1481	56.5	12.3	1250	2	Q4PIV2_USTWA	Q4piv2 ustilago ma
1482	56.5	12.3	1643	2	Q5ZCR4_ORYSA	Q5zcr4 oryza sativ
1483	56.5	12.3	1739	2	Q4SXM5_TETNG	Q4sxm5 tetraodon n
1484	56.5	12.3	1778	2	Q4IAN8_GIBZE	Q4ian8 gibberella
1485	56.5	12.3	1780	2	Q48F50_PSEI4	Q48p50 pseudomonas
1486	56.5	12.3	1838	2	Q6BCU9_TETTH	Q6bcj9 tetrahymena
1487	56.5	12.3	1844	2	Q5BDW2_EMENI	Q5bdw2 aspergillus
1488	56.5	12.3	2113	2	Q4RMA1_TETNG	Q4rma1 tetraodon n
1489	56.5	12.3	2217	1	DPOE_CANGA	Q6fnv7 candida gla
1490	56.5	12.3	2876	2	Q4Q573_LEIMA	Q4qb73 leishmania
1491	56.5	12.3	4464	2	Q7RL36_PLAYO	Q7rl36 plasmodium

1492	56	12.1	75	2	Q8E590_STR3	Q8e590 streptococc
1493	56	12.1	79	1	IVBKI_DENPO	P00981 dendroaspis
1494	56	12.1	100	2	Q6N984_RHOPA	Q6n984 rhodopseudo
1495	56	12.1	102	2	Q4AV09_9BURK	Q4av09 pollaromonas
1496	56	12.1	103	1	NIRC_PARDE	Q51702 paracoccus
1497	56	12.1	103	2	Q3PA73_PARDE	Q3pa73 paracoccus
1498	56	12.1	103	2	Q8K2N1_MOUSE	Q8k2n1 mus musculus
1499	56	12.1	117	2	Q3IPT2_NATPD	Q3ipt2 natronomona
1500	56	12.1	118	2	Q2JLN1_9CYAN	Q2jln1 cyanobacter

ALIGNMENTS

RESULT 1

Q6UWZ1_HUMAN PRELIMINARY; PRT; 89 AA.
ID Q6UWZ1_HUMAN PRELIMINARY; PRT; 89 AA.
AC Q6UWZ1;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE ERVTS26.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster H.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment."
RT bioinformatics assessment.
RL Genome Res. 13:2265-2270(2003).

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CC
CC EMBL; AY358584; AAQ8947.1; -; mRNA.
CC Ensembl; ENSG00000150201; Homo sapiens.
DR HGNC; HGNC:4028; FXFD4.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR000272; FXFD.
DR Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
DR PROSITE; PS01310; FXFD; 1.
SQ SEQUENCE 89 AA; 9433 MW; C5934288182449B0 CRC64;

Query Match	100.0%;	Score 461;	DB 2;	Length 89;
Best Local Similarity	100.0%;	Pred. No. 2.4e-41;		
Matches	89;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	MERTVLLALLLGLTALEANDPFANKDDPFYDWNKLNQLSGLICGGLAIAAGIAVL	SGK	60
Db	1	MERTVLLALLLGLTALEANDPFANKDDPFYDWNKLNQLSGLICGGLAIAAGIAVL	SGK	60
QY	61	CKYKSKQKQHSVPPEKAIPLITPGSATTC	89	
Db	61	CKYKSKQKQHSVPPEKAIPLITPGSATTC	89	

RESULT 2

1273	57	12.4	1574	2	Q7V5J5_9CAUD	Q7v5j5	xanthomonas	1346	56.5	12.3	316	2	Q2IRS6_RHOPA	Q2irs6	rhodopseudo
1274	57	12.4	1639	2	Q5A4J3_DICDI	Q5aj43	dictyosteli	1347	56.5	12.3	329	2	Q3LCU1_ACIAM	Q3lclj1	acidianus a
1275	57	12.4	1875	2	Q5X8U3_LEGOA	Q5x8u3	legionella	1348	56.5	12.3	335	2	Q8G6M8_BIFLO	Q8gcm8	bifidobacte
1276	57	12.4	2660	2	Q7QLI9_ANOPE	Q7qli9	anopheles g	1349	56.5	12.3	336	2	Q46PC3_RALEU	Q46pc3	raistonia e
1277	57	12.4	3196	2	Q6ALQ5_DESPS	Q6alq5	desulfotale	1350	56.5	12.3	337	1	TH23_TRYBB	Q09039	trypanosoma
1278	57	12.4	3338	2	Q82PH6_STREP	Q82ph6	streptomyce	1351	56.5	12.3	337	2	Q9GK55_RABIT	Q09k55	oryctolagus
1279	56.5	12.3	104	2	Q6J2H4_PSEYM	Q6j2h4	pseudomonas	1352	56.5	12.3	342	2	Q44BB6_SOLUS	Q44be6	solibacter
1280	56.5	12.3	107	2	Q67MA1_SYNTH	Q67ma1	symbiobacte	1353	56.5	12.3	342	2	Q46SJ4_RALEJ	Q46sj4	raistonia e
1281	56.5	12.3	110	2	Q6J932_9LILI	Q6j932	xerophyta h	1354	56.5	12.3	350	2	Q7UXC7_RHOBA	Q7uxc7	rhodopirell
1282	56.5	12.3	114	1	HXD3_RAT	P18867	rattus norv	1355	56.5	12.3	354	2	Q60DF9_ORYSA	Q60df9	oryza sativ
1283	56.5	12.3	118	2	Q3BH53_PLAFA	P18867	rattus norv	1356	56.5	12.3	354	2	Q4UKP7_RICFE	Q4ukp7	rickettsia
1284	56.5	12.3	120	2	Q6JIA6_HUMAN	Q6jia6	homo sapien	1357	56.5	12.3	358	2	Q2VQY9_ANAPL	Q2vqy9	anas platyr
1285	56.5	12.3	120	2	Q4MPP5_BACCCE	Q4mpp5	bacillus ce	1358	56.5	12.3	362	2	Q4P2I9_USTMA	Q4p2i9	ustilago ma
1286	56.5	12.3	120	2	Q63EVE_BACCZ	Q63eve	bacillus ce	1359	56.5	12.3	368	2	Q5YVA8_NOCFA	Q5yva8	nocardia fa
1287	56.5	12.3	120	2	Q8HMB7_BACHK	Q8hmb7	bacillus th	1360	56.5	12.3	372	2	Q5QNB2_ORYSA	Q5qnb2	oryza sativ
1288	56.5	12.3	120	2	Q8IU42_BACAN	Q8iu42	bacillus an	1361	56.5	12.3	374	2	Q5I7H1_NPVAP	Q5i7h1	atheraea p
1289	56.5	12.3	131	2	Q3DXU3_CHLAU	Q3dxu3	chloroflexu	1362	56.5	12.3	378	2	Q2RLI5_MOOTH	Q2rl15	moorella th
1290	56.5	12.3	143	2	Q8PLW5_XANAC	Q8plw5	xanthomonas	1363	56.5	12.3	387	2	Q88LL0_PSEPK	Q88ll0	pseudomonas
1291	56.5	12.3	145	2	Q75LT0_HUMAN	Q75lt0	homo sapien	1364	56.5	12.3	391	2	Q6MLC9_BDEBA	Q6mlc9	bdellovibri
1292	56.5	12.3	145	2	Q8E9G4_LYNST	Q8e9g4	lynnaea sta	1365	56.5	12.3	393	2	Q8IJG4_BACAN	Q8ijg4	bacillus an
1293	56.5	12.3	148	2	Q99LS0_MOUSE	Q99ls0	mus musculu	1366	56.5	12.3	394	2	Q7QAA4_ANOGA	Q7qea4	anopheles g
1294	56.5	12.3	148	2	Q9D2U7_MOUSE	Q9dzu7	m adult mal	1367	56.5	12.3	398	2	Q8LRB6_ORYSA	Q8lrbe6	oryza sativ
1295	56.5	12.3	167	2	Q34YP4_9GAMM	Q34yp4	alkalilimi	1368	56.5	12.3	403	2	Q7W0P4_BORPE	Q7w0p4	bordetella
1296	56.5	12.3	170	2	Q9W2N2_DROME	Q9w2n2	drosophila	1369	56.5	12.3	403	2	Q7W3G0_BORPA	Q7w3g0	bordetella
1297	56.5	12.3	178	2	Q2VW44_9LILI	Q2vw44	xerophyta h	1370	56.5	12.3	403	2	Q7WET0_BORBR	Q7wet0	bordetella
1298	56.5	12.3	186	2	Q6NL91_RHOPA	Q6nl91	rhodopseudo	1371	56.5	12.3	407	2	Q4J3Y8_AZOVI	Q4j3y8	azotobacter
1299	56.5	12.3	187	2	Q3YTK2_SHISS	Q3ytk2	shigella so	1372	56.5	12.3	408	2	Q8EIS5_SHEON	Q8eis5	shewanella
1300	56.5	12.3	187	2	Q52296_SHIFL	Q52296	shigella fl	1373	56.5	12.3	409	2	Q6LMI6_PHOPR	Q6lm16	photobacter
1301	56.5	12.3	187	2	Q7BEL2_SHIFL	Q7bel2	shigella fl	1374	56.5	12.3	411	2	Q7P149_CHRVO	Q7p149	chromobacte
1302	56.5	12.3	188	2	Q5FRN2_GLUOX	Q5frn2	gluconobact	1375	56.5	12.3	414	2	Q4BJH1_BURVI	Q4bjh1	burkholderi
1303	56.5	12.3	190	2	Q9JKW1_RAT	Q9jkw1	rattus norv	1376	56.5	12.3	414	2	Q4SS40_TETNG	Q4ss40	tetradon n
1304	56.5	12.3	191	2	Q5J7F1_SALCH	Q5j7f1	salmonella	1377	56.5	12.3	416	2	Q2X2D9_9GAMM	Q2x2d9	shewanella
1305	56.5	12.3	191	2	Q5PLD9_SALPA	Q5pld9	salmonella	1378	56.5	12.3	416	2	Q2ZQ35_SHEPU	Q2zq35	shewanella
1306	56.5	12.3	191	2	Q7CFP0_SALTY	Q7cfp0	salmonella	1379	56.5	12.3	416	2	Q3Q0H7_9GAMM	Q3q0h7	shewanella
1307	56.5	12.3	191	2	Q8XGY6_SALTI	Q8xgy6	salmonella	1380	56.5	12.3	416	2	Q44L75_CHRSL	Q44l75	chromohalob
1308	56.5	12.3	194	1	TIW22_MOUSE	Q9c85	mus musculu	1381	56.5	12.3	418	2	Q96JU9_HUMAN	Q96ju9	homo sapien
1309	56.5	12.3	194	2	Q5SSL1_MOUSE	O5sali	mus musculu	1382	56.5	12.3	419	1	CARP_CRYPA	P11838	cryphonectr
1310	56.5	12.3	194	2	Q9JKW2_MOUSE	Q9jkw2	mus musculu	1383	56.5	12.3	421	2	Q35Wk9_9GAMM	Q35wk9	shewanella
1311	56.5	12.3	195	2	Q8IN78_DROME	Q8in78	drosophila	1384	56.5	12.3	422	2	Q5PBS0_ANAMM	Q5pbs0	anaplasma m
1312	56.5	12.3	197	2	Q8U0L2_PYRFU	Q8u0l2	pyrococcus	1385	56.5	12.3	423	2	Q4D416_TRYCR	Q4d416	trypanosoma
1313	56.5	12.3	197	2	Q73KTE_TREDE	Q73kte6	treponema d	1386	56.5	12.3	428	2	Q59H29_HUMAN	Q59h29	homo sapien
1314	56.5	12.3	198	2	Q3R4M1_XYLFA	Q3r4m1	xyella fas	1387	56.5	12.3	436	2	Q41RQ0_FERAC	Q41rq0	ferroplasma
1315	56.5	12.3	198	2	Q3RFY3_XYLFA	Q3rfy3	xyella fas	1388	56.5	12.3	442	2	Q5QX17_IDILO	Q5qx17	idiomarina
1316	56.5	12.3	211	2	Q6EST5_FUGRU	Q6est5	fugu rubrip	1389	56.5	12.3	460	2	Q2RUB3_RHORU	Q2rub3	rhodospiril
1317	56.5	12.3	213	2	Q8NS64_CORGL	Q8ns64	corynebacte	1390	56.5	12.3	462	2	Q3IMJ0_SYNP7	Q3imj0	synecococc
1318	56.5	12.3	214	2	Q4V6C7_DROME	Q4v6c7	drosophila	1391	56.5	12.3	464	1	NORM_SYNBP	Q5mzd9	synecococc
1319	56.5	12.3	215	2	Q37HM5_RHOPA	Q37hm5	rhodopseudo	1392	56.5	12.3	468	2	Q2RUA2_RHORU	Q2rua2	rhodospiril
1320	56.5	12.3	228	2	Q84WK4_ARATH	Q84wk4	arabidopsis	1393	56.5	12.3	468	2	Q3JY99_BURPA	Q3jy99	burkholderi
1321	56.5	12.3	228	2	Q4A087_CHLLI	Q4ag87	chlorobium	1394	56.5	12.3	468	2	Q62G62_BURPA	Q62g62	burkholderi
1322	56.5	12.3	231	2	Q7ULW2_RHOBA	Q7ulw2	rhodopirell	1395	56.5	12.3	468	2	Q63PM6_BURPS	Q63pm6	burkholderi
1323	56.5	12.3	233	1	LPFX_MYCBO	P65307	mycobacteri	1396	56.5	12.3	471	2	Q49635_ARATH	Q49635	arabidopsis
1324	56.5	12.3	233	1	LPFX_MYCTU	P65306	mycobacteri	1397	56.5	12.3	472	2	Q2JN41_9CYAN	Q2jnn41	cyanobacter
1325	56.5	12.3	234	2	Q92LX9_RHIME	Q92lx9	rhizobium m	1398	56.5	12.3	484	2	Q55WA9_CRYNE	Q55wa9	cryptococcu
1326	56.5	12.3	240	2	Q3E033_CHLAU	Q3e033	chloroflexu	1399	56.5	12.3	484	2	Q4ZCK1_9CYAN	Q4zck1	bacterioph
1327	56.5	12.3	244	2	Q8K2G6_MOUSE	Q8k2g6	mus musculu	1400	56.5	12.3	484	2	Q8SDN4_9CAUD	Q8sdn4	staphylococ
1328	56.5	12.3	258	2	Q9HP14_HALSA	Q9hp14	halobacteri	1401	56.5	12.3	484	2	Q5HIX6_STAAC	Q5hix6	staphylococ
1329	56.5	12.3	269	2	Q4D929_TRYCR	Q4d929	trypanosoma	1402	56.5	12.3	484	2	Q8GG84_STAAR	Q8gg84	staphylococ
1330	56.5	12.3	269	2	Q4EID8_TRYCR	Q4eid8	trypanosoma	1403	56.5	12.3	485	2	Q7CZRT_AGRTS	Q7czrt7	agrobacteri
1331	56.5	12.3	274	2	Q4SET1_TETNG	Q4set1	tetradon n	1404	56.5	12.3	485	2	Q90YV3_XENLA	Q90y3	xenopus lae
1332	56.5	12.3	276	2	Q937L7_9CYAN	Q937l7	uncultured	1405	56.5	12.3	491	2	Q4PCU5_USTMA	Q4pcu5	ustilago ma
1333	56.5	12.3	276	2	Q937L8_9CYAN	Q937l8	uncultured	1406	56.5	12.3	494	2	Q86S12_9DPT	Q86s12	drosophila
1334	56.5	12.3	277	2	Q39UV6_GEONG	Q39uv6	geobacter m	1407	56.5	12.3	500	2	Q97KA2_CLOAB	Q97ka2	clostridium
1335	56.5	12.3	286	2	Q37UN3_SPHAR	Q37un3	novosphingo	1408	56.5	12.3	510	2	Q9RF10_MYXXA	Q9rf10	myxococcu
1336	56.5	12.3	288	2	Q38WC4_LACSS	Q38wc4	lactobacill	1409	56.5	12.3	511	1	ZGPAT_MOUSE	Q8vdm1	mus musculu
1337	56.5	12.3	288	2	Q826Y5_STRAW	Q826y5	streptomyce	1410	56.5	12.3	521	2	Q3TW85_MOUSE	Q3tw85	mus musculu
1338	56.5	12.3	292	2	Q3WVQ4_9RHIZ	Q3wvq4	mesorhizobi	1411	56.5	12.3	521	2	Q7RYH0_NEUCR	Q7ryh0	neurospora
1339	56.5	12.3	298	2	Q3F9W2_9BURK	Q3f9w2	burkholderi	1412	56.5	12.3	523	2	Q567M8_BRARE	Q567m8	brachydanio
1340	56.5	12.3	299	2	Q4SGT7_TETNG	Q4sgt7	tetradon n	1413	56.5	12.3	527	2	Q38AC0_9TRYP	Q38ac0	trypanosoma
1341	56.5	12.3	304	2	Q4H8A0_9DEIO	Q4h8a0	deinococcu	1414	56.5	12.3	528	2	Q38AB9_9TRYP	Q38ab9	trypanosoma
1342	56.5	12.3	304	2	Q2JDT3_9ACTO	Q2jdt3	frankia sp.	1415	56.5	12.3	529	1	TH2A_TRYBB	Q06222	trypanosoma
1343	56.5	12.3	305	2	Q52IU9_CHICK	Q52iu9	gallus gall	1416	56.5	12.3	529	2	Q38AB8_9TRYP	Q38ab8	trypanosoma
1344	56.5	12.3	308	2	Q3AYC0_SYNS9	Q3ayc0	synecococc	1417	56.5	12.3	533	2	Q3UFR6_MOUSE	Q3ufr6	mus musculu
1345	56.5	12.3	316	2	Q47SW6_THEFY	Q47sw6	thermobifid	1418	56.5	12.3	551	2	Q4JXL7_CORJK	Q4jxl7	corynebacte

1127	57	12.4	184	2	Q2NAP3_9SPHN	Q2nap3 erythroba	1200	57	12.4	457	2	Q325J8_SHIBS	Q325j8 shigella bo
1128	57	12.4	185	1	ADML_RAT	P43145 ratus norv	1201	57	12.4	457	2	Q32Jr4_SHIDS	Q32jf4 shigella dy
1129	57	12.4	190	1	PYRE_THETN	P58558 thermoanaer	1202	57	12.4	457	2	Q33SG9_SHIFL	Q33eg9 shigella fl
1130	57	12.4	192	2	Q3N6V0_9PROT	Q3n6v0 nitrosomona	1203	57	12.4	461	1	DCUC_ECO57	P0abp4 escherichia
1131	57	12.4	203	2	Q3VRW3_PROAE	Q3vrw3 prosthecoch	1204	57	12.4	461	1	DCUC_ECOLI	P0abp3 escherichia
1132	57	12.4	215	2	Q5COA4_SCHJA	Q5coa4 schistosoma	1205	57	12.4	461	1	DCUC_ECOLI	P0abp5 shigella fl
1133	57	12.4	228	2	Q83TM7_LISMO	Q83tm7 listeria mo	1206	57	12.4	461	1	DCUC_SHIFL	P0abp5 shigella fl
1134	57	12.4	230	2	Q8EG49_SHEON	Q8eg49 shewanella	1207	57	12.4	461	2	Q2T4W0_BURTH	P0abp5 shigella fl
1135	57	12.4	232	2	Q3TYU9_MOUSE	Q3tyu9 mus musculu	1208	57	12.4	461	2	Q324S1_SHIBS	Q324s1 shigella bo
1136	57	12.4	233	2	Q2YBT7_NITMU	Q2ybt7 nitrosospir	1209	57	12.4	461	2	Q395S6_BURS3	Q395s6 burkholderi
1137	57	12.4	241	2	Q658A8_ORYZA	Q658a8 oryza sativ	1210	57	12.4	461	2	Q3JFV9_BURP1	Q3jfv9 burkholderi
1138	57	12.4	249	2	Q3B7R5_BRARE	Q3b7r5 brachydanio	1211	57	12.4	461	2	Q57RU8_SALCH	Q57ru8 salmonella
1139	57	12.4	254	2	Q61095_TRYCR	Q61095 trypanosoma	1212	57	12.4	461	2	Q63M54_BURPS	Q63m54 burkholderi
1140	57	12.4	254	2	Q3FST5_9BURK	Q3fst5 rhodofexax	1213	57	12.4	468	2	Q7QD04_ANOGA	Q7qd04 anopheles g
1141	57	12.4	258	1	UDP_TREPA	Q83990 treponema p	1214	57	12.4	470	2	Q3A4E3_PELCD	Q3a4e3 pelobacter
1142	57	12.4	264	2	Q46QR2_RALEJ	Q46qr2 ralistonia e	1215	57	12.4	471	2	Q5JNB5_ORYSA	Q5jnb5 oryza sativ
1143	57	12.4	268	2	Q70FH9_9CVAN	Q70fh9 uncultured	1216	57	12.4	477	2	Q83TQ3_LISMO	Q83tq3 listeria mo
1144	57	12.4	269	2	Q8YQW0_ANASP	Q8yqw0 anabaena sp	1217	57	12.4	477	2	Q84DP6_LISMO	Q84dp6 listeria mo
1145	57	12.4	276	2	Q68ES3_XENIA	Q68es3 xenopus lae	1218	57	12.4	477	2	Q84DP7_LISMO	Q84dp7 listeria mo
1146	57	12.4	281	2	Q3OWE1_DESDG	Q3owe1 desulfovibr	1219	57	12.4	477	2	Q84DP8_LISMO	Q84dp8 listeria mo
1147	57	12.4	283	2	Q4V7U2_XENLA	Q4v7u2 xenopus lae	1220	57	12.4	477	2	Q84DP9_LISMO	Q84dp9 listeria mo
1148	57	12.4	287	2	Q41VJ1_DESHA	Q41vj1 desulfitoba	1221	57	12.4	477	2	Q84DQ0_LISMO	Q84dq0 listeria mo
1149	57	12.4	289	2	Q2XIL5_PSPPU	Q2xil5 pseudomonas	1222	57	12.4	477	2	Q722W8_LISMF	Q722w8 listeria mo
1150	57	12.4	291	2	Q5WX66_LEGPL	Q5wx66 legionella	1223	57	12.4	478	2	Q84DN9_LISMO	Q84dn9 listeria mo
1151	57	12.4	292	2	Q6UY47_HUMAN	Q6uy47 homo sapien	1224	57	12.4	478	2	Q84DS7_LISMO	Q84ds7 listeria mo
1152	57	12.4	292	2	Q3P8A6_PARDE	Q3p8a6 paracoccu	1225	57	12.4	479	2	Q2K3U6_RHET	Q2k3u6 rhizobium e
1153	57	12.4	301	2	Q8BYJ2_MOUSE	Q8byj2 m adult mal	1226	57	12.4	487	1	P8BC_PORPU	P51356 porphyra pu
1154	57	12.4	302	2	Q2ZQT2_SHEPU	Q2zqt2 shewanella	1227	57	12.4	487	2	Q8H1D7_ARATH	Q8h1d7 arabidopsis
1155	57	12.4	302	2	Q2ZSJ9_SHEPU	Q2zsj9 shewanella	1228	57	12.4	487	2	Q93ZU2_ARATH	Q93zu2 arabidopsis
1156	57	12.4	302	2	Q768S4_MOUSE	Q768s4 mus musculu	1229	57	12.4	493	2	Q7NC13_MYCGA	Q7nc13 mycobact
1157	57	12.4	305	2	Q2X7G0_9GAMM	Q2x7g0 shewanella	1230	57	12.4	494	1	ILVC_PHOPE	Q61vz5 photobacter
1158	57	12.4	313	2	Q3OWA0_DESDG	Q3owa0 desulfovibr	1231	57	12.4	499	2	Q3J6V4_NITOC	Q3j6v4 nitrococc
1159	57	12.4	315	2	Q9UNE2_HUMAN	Q9une2 homo sapien	1232	57	12.4	516	2	Q37V73_SHAR	Q37v73 novosphingo
1160	57	12.4	325	2	Q9QN99_9VIRU	Q9qn99 rice grassy	1233	57	12.4	517	2	Q2XM06_PSEPU	Q2xm06 pseudomonas
1161	57	12.4	332	2	Q52M67_PAVLU	Q52m67 pavlova lut	1234	57	12.4	517	2	Q8EGW6_PSEPK	Q8egw6 pseudomonas
1162	57	12.4	334	2	Q52W83_BANAT	Q52w83 bangia atro	1235	57	12.4	531	2	Q6OVX5_CAEBR	Q6ovx5 caenorhabdi
1163	57	12.4	342	1	ISIA_SINP6	Q5n575 synchococc	1236	57	12.4	534	2	Q4WG10_ASPFR	Q4wg10 aspergillus
1164	57	12.4	342	1	ISIA_SINP7	P15347 synchococc	1237	57	12.4	535	2	Q4KIR3_PSEF5	Q4kir3 pseudomonas
1165	57	12.4	342	2	Q31MZ7_SINP7	Q3lmz7 synchococc	1238	57	12.4	551	2	Q3SFN7_THIDA	Q3sfn7 thioabacillu
1166	57	12.4	343	2	Q5LM56_SILPO	Q5lm56 silicibacte	1239	57	12.4	555	2	Q2UBA3_ASPOR	Q2uba3 aspergillus
1167	57	12.4	351	2	Q97774_FELCA	Q97774 felis silve	1240	57	12.4	555	2	Q8BYE8_MOUSE	Q8bye8 mus musculu
1168	57	12.4	352	2	Q867D6_FELCA	Q867d6 felis silve	1241	57	12.4	576	2	Q8BAM8_PSESM	Q8bam8 pseudomonas
1169	57	12.4	353	2	Q9LR37_ARATH	Q9lr37 arabidopsis	1242	57	12.4	606	2	Q7Z2H9_HUMAN	Q7z2h9 homo sapien
1170	57	12.4	355	2	Q5QNA9_ORYSA	Q5qna9 oryza sativ	1243	57	12.4	610	2	Q8N695_HUMAN	Q8n695 homo sapien
1171	57	12.4	360	2	Q8WBK3_9AVES	Q8wbk3 saurothera	1244	57	12.4	610	2	Q2TB99_HUMAN	Q2tb99 homo sapien
1172	57	12.4	372	2	Q2JJC4_9CVAN	Q2jjc4 cyanobacter	1245	57	12.4	629	2	Q4I3Y7_GIBZE	Q4i3y7 gibberella
1173	57	12.4	374	2	Q80638_ARATH	Q80638 arabidopsis	1246	57	12.4	633	2	Q746H7_THET2	Q746h7 thermus the
1174	57	12.4	374	2	Q672B8_ARATH	Q672b8 arabidopsis	1247	57	12.4	661	2	Q8MJD4_RABIT	Q8mjd4 oryctolagus
1175	57	12.4	374	2	Q9SVF3_ARATH	Q9svf3 arabidopsis	1248	57	12.4	661	2	Q2KB68_RHET	Q2kb68 rhizobium e
1176	57	12.4	374	2	Q2WCM8_LISMO	Q2wcm8 listeria mo	1249	57	12.4	679	2	Q4QI11_DESAC	Q4qi11 desulfurom
1177	57	12.4	374	2	Q5NXXV2_AZOSE	Q5nxxv2 azoarcus sp	1250	57	12.4	689	2	Q6A4I8_BUTFI	Q6a4i8 butyriibri
1178	57	12.4	376	2	Q6FV38_CANGA	Q6fv38 candida gla	1251	57	12.4	699	2	Q7N1I1_GLOVI	Q7n1i1 gloebacter
1179	57	12.4	383	2	Q6HGU3_BACHK	Q6hgu3 bacillus th	1252	57	12.4	705	2	Q4T7V1_TETNG	Q4t7v1 tetraodon n
1180	57	12.4	383	2	Q81NM9_BACAN	Q81nm9 bacillus an	1253	57	12.4	773	2	Q2RYC4_RHORA	Q2ryc4 rhodospiril
1181	57	12.4	384	2	Q65X10_ORYSA	Q65x10 oryza sativ	1254	57	12.4	779	2	Q37V54_SPHAR	Q37v54 novosphingo
1182	57	12.4	385	2	Q9S2G0_ARATH	Q9s2g0 arabidopsis	1255	57	12.4	792	2	Q4RXC8_TETNG	Q4rxc8 tetraodon n
1183	57	12.4	386	2	Q5NFP0_FRAIT	Q5nfp0 francisella	1256	57	12.4	802	2	Q7UMP8_RHOBA	Q7ump8 rhodopirell
1184	57	12.4	387	2	Q5B694_EMENI	Q5b694 aspergillus	1257	57	12.4	811	2	Q4FXZ2_LEIMA	Q4fxz2 leishmania
1185	57	12.4	387	2	Q6AOC8_DESPS	Q6aoc8 desulfotale	1258	57	12.4	858	2	Q6ZPE7_MOUSE	Q6zpe7 mus musculu
1186	57	12.4	394	2	Q47B29_DECAR	Q47b29 dechloromon	1259	57	12.4	880	2	Q6KI07_MYCMO	Q6ki07 mycobact
1187	57	12.4	399	2	Q53J03_SHIFL	Q53j03 shigella fl	1260	57	12.4	892	2	Q5LJMB_SILPO	Q5ljmb silicibacte
1188	57	12.4	404	2	Q2IMU0_9DELT	Q2imu0 anaeromxob	1261	57	12.4	953	1	PRF40_MOUSE	Q9rlc7 mus musculu
1189	57	12.4	409	2	Q639H1_BACCZ	Q639h1 bacillus ce	1262	57	12.4	1056	2	Q2E227_XANOR	Q2e227 xanthomonas
1190	57	12.4	425	2	Q2N773_9SPHN	Q2n773 erythroba	1263	57	12.4	1056	2	Q5GZ12_XANOR	Q5gzi12 xanthomonas
1191	57	12.4	440	2	Q9LMU8_ARATH	Q9lm8 arabidopsis	1264	57	12.4	1068	2	Q2W307_MAGSA	Q2w307 magnetospir
1192	57	12.4	440	2	Q8BJG0_MOUSE	Q8bjg0 mus musculu	1265	57	12.4	1137	2	Q82E10_STRAW	Q82e10 streptomyce
1193	57	12.4	447	2	Q3Z4H2_SHISS	Q3z4h2 shigella so	1266	57	12.4	1141	2	Q2OKJ9_BRARE	Q2okj9 brachydanio
1194	57	12.4	456	1	PROY_ECOL6	P0aae4 escherichia	1267	57	12.4	1151	2	Q754S3_ASHGO	Q754s3 ashya goss
1195	57	12.4	457	1	PROY_ECOL6	P0aae3 escherichia	1268	57	12.4	1185	2	Q3QC38_9GAMM	Q3qc38 shewanella
1196	57	12.4	457	1	PROY_ECOL6	P0aae2 escherichia	1269	57	12.4	1213	2	Q443X7_SOLUS	Q443x7 solibacter
1197	57	12.4	457	1	PROY_ECOL6	P0aae2 escherichia	1270	57	12.4	1294	2	Q50HM7_STRSH	Q50hm7 streptomyce
1198	57	12.4	457	2	Q3Z507_SHISS	Q3z507 shigella so	1271	57	12.4	1491	2	Q5GF21_HABIN	Q5gf21 haemophilus
1199	57	12.4	457	2	Q2MC24_ECOLI	Q2mc24 escherichia	1272	57	12.4	1571	2	Q2NPH0_9CAUD	Q2nph0 xanthomonas

981	58	12.6	1135	2	Q9VTB8_DROME	Q9vtb8	drosophila	1054	57.5	12.5	446	2	Q6H703_ORYSA	O6h7q3	oryza sativ
982	58	12.6	1149	2	Q7KUE4_DROME	Q7kue4	drosophila	1055	57.5	12.5	448	2	Q6NBL7_RHOPA	Q6nbl7	rhodopseudo
983	58	12.6	1185	2	Q2ZX48_SHEPU	Q2zx48	shewanella	1056	57.5	12.5	453	2	Q7ZVN2_BRARE	Q7zvn2	brachydanio
984	58	12.6	1189	2	Q3VP02_9CHLB	Q3vp02	pelodictyon	1057	57.5	12.5	461	2	Q35RR8_9BRAD	Q35rr8	bradyrhizob
985	58	12.6	1430	2	Q33169_METHU	Q33169	methanospir	1058	57.5	12.5	461	2	Q35PM91_SALPA	Q35pm91	salmonella
986	58	12.6	1477	2	Q3M3M6_ANAVT	Q3m3m6	anabaena va	1059	57.5	12.5	461	2	Q65QV2_MANSMA	Q65qv2	mannheimia
987	58	12.6	1621	2	Q7PQL1_ANOGA	Q7pql1	anopheles g	1060	57.5	12.5	461	2	Q916B1_PSEAR	Q916el	pseudomonas
988	58	12.6	1805	2	Q9XTP6_PLABE	Q9xtp6	plasmodium	1061	57.5	12.5	461	2	Q8Z815_SALTI	Q8z8is	salmonella
989	58	12.6	2576	2	Q8JFV5_BRARE	Q8jfv5	brachydanio	1062	57.5	12.5	473	2	Q2J897_9CYAN	Q2j897	cyanobacter
990	58	12.6	4836	2	Q88473_MOUSE	Q88473	mus musculus	1063	57.5	12.5	502	2	Q5V1D8_HALMA	Q5v1d8	haloarcu
991	58	12.6	4836	2	Q4U2R1_MOUSE	Q4u2r1	mus musculus	1064	57.5	12.5	507	2	Q5PPF5_RAT	Q5ppf5	rattus norv
992	57.5	12.5	71	1	V1RT62_XENLA	P19011	xenopus lae	1065	57.5	12.5	517	2	Q8EV45_MYCPE	Q8ev45	mycoplasma
993	57.5	12.5	84	2	Q8T6F5_DROPS	Q8t6f5	drosophila	1066	57.5	12.5	523	2	Q916Z6_PSEAE	Q916z6	pseudomonas
994	57.5	12.5	106	2	Q3J6Q5_NITOC	Q3j6q5	nitrosococc	1067	57.5	12.5	528	1	KCNA3_MOUSE	P16390	mus musculu
995	57.5	12.5	128	2	Q9NG96_MAMBR	Q9ng96	amestra br	1068	57.5	12.5	531	2	Q8ERG1_OCEIH	Q8erg1	oceanobacil
996	57.5	12.5	129	2	Q4K8V9_PSEF5	Q4k8v9	pseudomonas	1069	57.5	12.5	541	2	Q4SFX1_TETNG	Q4sfx1	tetradoon n
997	57.5	12.5	133	2	Q3GWD4_9ACTO	Q3gwd4	nocardioide	1070	57.5	12.5	545	2	Q3H6F9_9ACTO	Q3h6f9	nocardioide
998	57.5	12.5	139	2	Q8Z6V7_SALTI	Q8z6v7	salmonella	1071	57.5	12.5	574	2	Q8XQ27_RALSO	Q8xq27	raletonia s
999	57.5	12.5	144	2	Q5YXC3_NOCFA	Q5yxc3	nocardia fa	1072	57.5	12.5	581	2	Q6BK68_DEBHA	Q6bk68	debaromyce
1000	57.5	12.5	144	2	Q9ERF0_RAT	Q9erf0	rattus norv	1073	57.5	12.5	581	2	Q3JDR2_NITOC	Q3jdr2	nitrosococc
1001	57.5	12.5	146	2	Q5LS51_SILPO	Q5lse1	silicibacte	1074	57.5	12.5	594	2	Q98PX5_MYCPU	Q98px5	mycoplasma
1002	57.5	12.5	153	2	Q8K071_MOUSE	Q8k071	mus musculus	1075	57.5	12.5	603	2	Q4P4K6_USTMA	Q4p4k6	ustilago ma
1003	57.5	12.5	160	2	Q3NYQ1_9GAMM	Q3nyq1	shewanella	1076	57.5	12.5	636	2	Q86486_9PARA	Q86486	rinderpest
1004	57.5	12.5	173	2	Q85CX0_9TELE	Q85cx0	salangichch	1077	57.5	12.5	656	2	Q8K244_MOUSE	Q8k244	mus musculu
1005	57.5	12.5	184	2	Q5U4U5_XENLA	Q5u4u5	xenopus lae	1078	57.5	12.5	662	1	HEPA_HHV6Z	P52451	human herpe
1006	57.5	12.5	194	1	T1W222_BOVIN	Q5b1n4	bos taurus	1079	57.5	12.5	662	2	Q9WT01_9BETA	Q9wt01	human herpe
1007	57.5	12.5	208	2	Q3QVC0_9RHOB	Q3qvc0	silicibacte	1080	57.5	12.5	668	2	Q4UXH5_XANON	Q4uxh5	xanthomonas
1008	57.5	12.5	224	1	CLPPI1_SYNPH	Q7ua36	synthococc	1081	57.5	12.5	668	2	Q8P6N7_XANCP	Q8p6n7	xanthomonas
1009	57.5	12.5	232	2	Q3SN04_NITWN	Q3sn04	nitrobacter	1082	57.5	12.5	670	2	Q9BAQ4_9WAGN	Q9baq4	buxus citri
1010	57.5	12.5	242	2	Q8J3T33_SALTI	Q8j3t33	salmonella	1083	57.5	12.5	671	2	Q5AKV5_CANAL	Q5akv5	candida alb
1011	57.5	12.5	255	2	Q7XQ06_ORYSA	Q7xq06	oryza sativ	1084	57.5	12.5	690	2	Q2QY62_ORYSA	Q2qy62	oryza sativ
1012	57.5	12.5	262	2	Q4B6Y1_BURVI	Q4b6y1	burkholderi	1085	57.5	12.5	692	2	Q9BAR1_9WAGN	Q9bar1	buxus glome
1013	57.5	12.5	267	2	Q3V9M8_9SPHN	Q3v9m8	spalingoxyxi	1086	57.5	12.5	745	1	PURL_HELHP	Q7vif52	helicobacte
1014	57.5	12.5	281	2	Q4AES7_9CHLB	Q4aes7	chlorobium	1087	57.5	12.5	750	2	Q519G2_ENTHI	Q519g2	entamoeba h
1015	57.5	12.5	284	2	Q4A5Z3_MYCS5	Q4a5z3	mycoplasma	1088	57.5	12.5	771	2	Q617U6_CAEBR	Q617u6	caenorhabdi
1016	57.5	12.5	292	2	Q6FUC0_CANGA	Q6fuc0	candida gla	1089	57.5	12.5	772	2	Q75JP4_DICDI	Q75jp4	dictyosteli
1017	57.5	12.5	301	2	Q4CG95_CLOTM	Q4cg95	clostridium	1090	57.5	12.5	794	2	Q6GP40_XENLA	Q6gp40	xenopus lae
1018	57.5	12.5	307	2	Q46720_ECOLI	Q46720	escherichia	1091	57.5	12.5	796	2	Q2M106_DROPS	Q2m106	drosophila
1019	57.5	12.5	313	2	Q7NWF7_CHRVO	Q7nwf7	chromobacte	1092	57.5	12.5	822	2	Q8IQN2_DROME	Q8iqn2	drosophila
1020	57.5	12.5	320	2	Q423R8_DESHA	Q423r8	desulfovib	1093	57.5	12.5	857	1	OPGH_PSEPK	Q88q02	pseudomonas
1021	57.5	12.5	323	2	Q93H09_STRAW	Q93h09	streptomyce	1094	57.5	12.5	857	2	Q2XJ39_PSEPU	Q2xj39	pseudomonas
1022	57.5	12.5	324	2	Q9S248_STRCO	Q9s248	streptomyce	1095	57.5	12.5	865	2	Q61J98_CAEBR	Q61j98	caenorhabdi
1023	57.5	12.5	325	2	Q4C1H7_CROWT	Q4c1h7	crocospaer	1096	57.5	12.5	882	2	Q8MQK2_DROME	Q8mqk2	drosophila
1024	57.5	12.5	325	2	Q2J1H8_9CYAN	Q2j1h8	cyanobacter	1097	57.5	12.5	907	2	Q8VY10_ARATH	Q8vy10	arabidopsis
1025	57.5	12.5	328	2	Q4B500_9BURK	Q4b500	polaromonas	1098	57.5	12.5	993	2	Q3JBQ7_NITOC	Q3jbq7	nitrosococc
1026	57.5	12.5	337	2	Q817B2_FASHE	Q817b2	fasciola he	1099	57.5	12.5	1012	2	Q8XUM5_RALSO	Q8xum5	raletonia s
1027	57.5	12.5	342	1	ISIA_STNP2	P31157	synthococc	1100	57.5	12.5	1071	2	Q993F2_9GAMA	Q993f2	callitrichi
1028	57.5	12.5	346	2	Q34ZU6_9GAMM	Q34zu6	alkalilimi	1101	57.5	12.5	1151	2	Q30WB9_DSDDG	Q30wb9	desulfovibr
1029	57.5	12.5	353	2	Q9LRS5_9ARATH	Q9lrs5	arabidopsis	1102	57.5	12.5	1625	2	Q6MVD4_NFUCR	Q6mvd4	neurospora
1030	57.5	12.5	355	2	Q4JFC3_MOUSE	Q4jfc3	mus musculus	1103	57.5	12.5	1681	2	Q4SVT8_TETNG	Q4svt8	tetradoon n
1031	57.5	12.5	356	2	Q9Y941_AEROPE	Q9y941	aeropyrum p	1104	57.5	12.5	1696	2	Q4N0K7_THEPA	Q4n0k7	theileria p
1032	57.5	12.5	363	1	MURG_ERECT	Q6d013	erwinia car	1105	57.5	12.5	1751	2	Q57V95_9TRYP	Q57v95	trypanosoma
1033	57.5	12.5	371	2	Q53GK2_HUMAN	Q53gk2	homo sapien	1106	57.5	12.5	1902	1	P2P_LACPA	Q02470	lactobacill
1034	57.5	12.5	371	2	Q9J8C7_9NUCL	Q9j8c7	spodoptera	1107	57.5	12.5	1919	2	Q38FO7_9TRYP	Q38fo7	trypanosoma
1035	57.5	12.5	374	1	OE56_NFVOP	Q83953	orgyia pseu	1108	57.5	12.5	2235	1	CHD7_HUMAN	Q9p2d1	homo sapien
1036	57.5	12.5	379	1	MCF_CAVPO	P70105	cavia porce	1109	57.5	12.5	2322	1	SDK_CAEBR	Q6zn5	caenorhabdi
1037	57.5	12.5	380	2	Q3FL66_9BURK	Q3fl66	rhodofera	1110	57.5	12.5	3300	2	Q4N127_THEPA	Q4n127	theileria p
1038	57.5	12.5	381	2	Q3GHP7_CHLVI	Q3ghp7	prosthococh	1111	57	12.4	93	2	Q48AY6_PSE14	Q48ay6	pseudomonas
1039	57.5	12.5	382	2	Q3AHL8_SYNSC	Q3ahl8	synthococc	1112	57	12.4	100	2	Q37KZ7_RHOPA	Q37kz7	rhodopseudo
1040	57.5	12.5	383	2	Q8A186_BACTN	Q8a186	bacteroides	1113	57	12.4	105	2	Q48B09_PSE14	Q48b09	pseudomonas
1041	57.5	12.5	385	2	Q3FBP6_9BURK	Q3fbf6	burkholderi	1114	57	12.4	105	2	Q4FT10_PSYAR	Q4ft10	psychobact
1042	57.5	12.5	386	2	Q2W1P7_MAGSA	Q2w1p7	magnetospir	1115	57	12.4	134	2	Q43SW8_SOLUS	Q43sw8	solibacter
1043	57.5	12.5	388	2	Q54466_STRMV	Q54466	streptomyce	1116	57	12.4	148	2	Q8LGH9_ARATH	Q8lgh9	arabidopsis
1044	57.5	12.5	401	2	Q874Z7_PODAN	Q874z7	podospora a	1117	57	12.4	148	2	Q92V24_ARATH	Q92v24	arabidopsis
1045	57.5	12.5	402	2	Q727Q2_HUMAN	Q727q2	homo sapien	1118	57	12.4	152	2	Q8E595_STRAT	Q8e595	streptococc
1046	57.5	12.5	404	2	Q3CSM6_ALTAT	Q3csm6	pseudocalter	1119	57	12.4	153	2	Q3GVV6_9ACTO	Q3gvv6	nocardioide
1047	57.5	12.5	416	2	Q2ZDB2_9GAMM	Q2zdb2	shewanella	1120	57	12.4	158	2	Q6FSW5_CANGA	Q6fsw5	candida gla
1048	57.5	12.5	416	2	Q35YTI_9GAMM	Q35yti	shewanella	1121	57	12.4	158	2	Q4AVP7_9BURK	Q4avp7	polaromonas
1049	57.5	12.5	426	2	Q57137_9BETA	Q57137	human herpe	1122	57	12.4	160	2	Q3H7T3_TRIER	Q3h7t3	trichodesmi
1050	57.5	12.5	427	2	Q3PE38_PARDE	Q3pe38	paracoccus	1123	57	12.4	166	2	Q61JJI_DROME	Q61jj1	drosophila
1051	57.5	12.5	433	2	Q4H838_9DEIO	Q4h838	deinococcus	1124	57	12.4	173	2	Q45RH2_BRARE	Q45rh2	brachydanio
1052	57.5	12.5	441	2	Q60NJ4_CAEBR	Q60nj4	caenorhabdi	1125	57	12.4	177	2	Q5LKW5_SILPO	Q5lkw5	silicibacte
1053	57.5	12.5	441	2				1126	57	12.4	184	2	Q8LE27_ARATH	Q8le27	arabidopsis

835	58.5	12.7	482	2	Q97CF4_THERVO	Q97cf4 thermoplas	908	58	12.6	331	2	Q65F35_BACLD	Q65f35 bacillus li
836	58.5	12.7	492	2	Q2UR56_ASPOR	Q2ur56 aspergillus	909	58	12.6	333	2	Q8N7W6_HUMAN	Q8n7w6 homo sapien
837	58.5	12.7	499	2	Q4NDZ1_9MICC	Q4ndz1 arthroba	910	58	12.6	338	2	Q3GNL5_9GAMM	Q3gnl5 psychobact
838	58.5	12.7	509	2	Q58NS5_9TRYP	Q58ns5 trypanosoma	911	58	12.6	338	2	Q2VRR2_ANAPL	Q2vrr2 anas platyr
839	58.5	12.7	516	2	Q84DM1_LISSE	Q84dm1 listeria se	912	58	12.6	344	2	Q4V1K5_BACCZ	Q4v1k5 bacillus ce
840	58.5	12.7	516	2	Q84DU3_LISSE	Q84du3 listeria se	913	58	12.6	344	2	Q6AXV5_RAT	Q6axv5 rattus norv
841	58.5	12.7	557	2	Q8VZE2_ARATH	Q8vze2 arabidopsis	914	58	12.6	345	1	ARGC_BACAN	Q8lmg95 bacillus an
842	58.5	12.7	565	2	Q83DB5_COXBU	Q83db5 coxiella bu	915	58	12.6	349	2	Q7MGC8_VIBVY	Q7mgc8 vibrio vuln
843	58.5	12.7	570	2	Q3WTT0_9RHIZ	Q3wtt0 mesorhizobi	916	58	12.6	354	2	Q95HB3_ANAPL	Q95hb3 anas platyr
844	58.5	12.7	586	2	Q21Z98_RHOPA	Q21z98 rhodopseudo	917	58	12.6	368	2	Q23311_CABEL	Q23311 caenorhabdi
845	58.5	12.7	587	2	Q46RL3_RALEJ	Q46rl3 ralstonia e	918	58	12.6	369	2	Q3CML7_ALTAT	Q3cm17 pseudocalt
846	58.5	12.7	587	2	Q91A29_ONCWM	Q91a29 oncorhynch	919	58	12.6	376	2	Q3W5W5_9ACTO	Q3w5w5 frankia sp.
847	58.5	12.7	615	2	Q3GQAL_9GAMM	Q3gqal psychobact	920	58	12.6	369	2	Q926X9_LISIN	Q926x9 listeria in
848	58.5	12.7	633	2	Q9LMNH_4ARATH	Q9lmnh arabidopsis	921	58	12.6	383	2	Q1BNS_5BACC	Q1bn5 bacillus ce
849	58.5	12.7	639	2	Q4HWW9_GIBZE	Q4hww9 gibberella	922	58	12.6	387	2	Q3KQD5_MOUSE	Q3kqd5 mus muscul
850	58.5	12.7	652	2	Q6VTW8_NPVCD	Q6vtw8 choristoneu	923	58	12.6	390	2	Q3EJR8_BACTI	Q3ejr8 bacillus th
851	58.5	12.7	679	2	Q4C8Q3_CROWT	Q4c8q3 cryptosphaer	924	58	12.6	395	2	Q7PSF3_ANOGA	Q7psf3 anopheles g
852	58.5	12.7	683	2	Q5CN79_CRYHO	Q5cn79 cryospori	925	58	12.6	398	1	SELI_MOUSE	Q80tal mus muscul
853	58.5	12.7	685	2	Q367G1_9GAMM	Q367g1 shewanella	926	58	12.6	398	2	Q9KPH1_VIBCH	Q9kph1 vibrio chol
854	58.5	12.7	716	2	Q53UCB_WHEAT	Q53ucb triticum ae	927	58	12.6	403	2	Q5F7W0_NRIGI	Q5f7w0 neisseria g
855	58.5	12.7	716	2	Q58QF6_WHEAT	Q58qf6 triticum ae	928	58	12.6	409	2	Q4MX56_BACCE	Q4mx56 bacillus ce
856	58.5	12.7	719	2	Q89ZF6_WHEAT	Q89zf6 bacteroides	929	58	12.6	411	2	Q7YQP7_OCHPR	Q7yqp7 ochotona pr
857	58.5	12.7	726	2	Q89ZN6_BACTN	Q89zn6 bacteroides	930	58	12.6	425	2	Q3C7K5_9CLOT	Q3c7k5 alkaliphilu
858	58.5	12.7	731	2	Q8HTN2_9MAGN	Q8htn2 ranzania ja	931	58	12.6	429	2	Q3B2J5_PELLD	Q3b2j5 peiodictyon
859	58.5	12.7	733	2	Q37R00_SPHAR	Q37r00 novosphingo	932	58	12.6	440	2	Q4MSY3_BACCE	Q4msy3 bacillus ce
860	58.5	12.7	807	2	Q3NN16_SHEFR	Q3nn16 shewanella	933	58	12.6	440	2	Q63DG6_BACCZ	Q63dg6 bacillus ce
861	58.5	12.7	818	2	Q380A5_SPHAR	Q380a5 novosphingo	934	58	12.6	440	2	Q6HKY9_BACHK	Q6hky9 bacillus th
862	58.5	12.7	876	1	SYL_NEIMB	Q3pk62 paracoccus	935	58	12.6	440	2	Q81FL1_BACCR	Q81fl1 bacillus ce
863	58.5	12.7	878	2	Q5FAJ3_NEIG1	Q5faj3 neisseria m	936	58	12.6	440	2	Q81SQ4_BACAN	Q81sq4 bacillus ce
864	58.5	12.7	1048	2	Q6EMD9_ECOLI	Q6emd9 escherichia g	937	58	12.6	440	2	Q73AS4_BACC1	Q73as4 bacillus ce
865	58.5	12.7	1048	2	Q6UEN9_KLEPN	Q6uen9 klebsiella	938	58	12.6	444	2	Q4SMG6_TTTNG	Q4smg6 tetraodon n
866	58.5	12.7	1105	2	Q9CFH5_ARATH	Q9cfh5 arabidopsis	939	58	12.6	458	2	Q84DP2_LISMO	Q84dp2 listeria mo
867	58.5	12.7	1105	2	Q5F3N7_CHICK	Q5f3n7 gallus gall	940	58	12.6	457	2	Q4KJP7_PSEFS	Q4kjp7 pseudomonas
868	58.5	12.7	1140	2	Q33RL7_9GAMM	Q33rl7 shewanella	941	58	12.6	461	2	Q8ZR07_SALTY	Q8zr07 salmonella
869	58.5	12.7	1189	2	Q44A15_9RHIZ	Q44a15 agrobacteri	942	58	12.6	462	2	Q9RYH5_DEIRA	Q9ryh5 deinococcus
870	58.5	12.7	1720	2	Q4FXS8_LEIMA	Q4fxs8 leishmania	943	58	12.6	486	2	Q6DBW3_BRARE	Q6dbw3 brachydanio
871	58.5	12.7	1817	2	Q7SZF6_XENIA	Q7szf6 xenopus lae	944	58	12.6	487	2	Q4T7M0_TTTNG	Q4t7m0 tetraodon n
872	58.5	12.7	2473	2	Q9SLC7_5MAMM	Q9slc7 tachyglossu	945	58	12.6	511	2	Q74CB3_GEOSL	Q74cb3 geobacter s
873	58.5	12.7	2710	2	Q8T3G9_CABEL	Q8t3g9 caenorhabdi	946	58	12.6	541	2	Q21L02_9BELT	Q21l02 anaeromyxob
874	58.5	12.7	2712	2	Q01808_CABEL	Q01808 caenorhabdi	947	58	12.6	548	2	Q4TKP3_BURTH	Q4tkp3 burkholderi
875	58.5	12.7	5359	2	Q5VKR4_SACER	Q5vkr4 saccharopol	948	58	12.6	549	2	Q4DSC2_TRYCR	Q4dsc2 trypanosoma
876	58.5	12.7	6193	2	Q8KSQ0_STRCP	Q8ksq0 streptomyce	949	58	12.6	549	2	Q8GGR2_STRAZ	Q8ggr2 streptomyc
877	58	12.6	89	2	Q3SPX3_NITWN	Q3spx3 nitrobacter	950	58	12.6	549	2	Q8GGR2_STRAZ	Q8ggr2 streptomyc
878	58	12.6	96	2	Q83E08_COXBU	Q83e08 coxiella bu	951	58	12.6	551	2	Q2UPK5_ASPOR	Q2upk5 aspergillus
879	58	12.6	104	2	Q24949_FASHE	Q24949 fasciola he	952	58	12.6	552	2	Q4J3Z2_AZOVI	Q4j3z2 azotobacter
880	58	12.6	113	2	Q3ULC1_MOUSE	Q3ulc1 mus musculu	953	58	12.6	553	2	Q94ZJ6_ORYSA	Q94zj6 oryza sativ
881	58	12.6	114	1	YDGO_BAGSU	P96702 bacillus su	954	58	12.6	614	2	Q7UVX4_RHOBA	Q7uvx4 rhodopirell
882	58	12.6	120	2	Q4J5Z8_AZOVI	Q4j5z8 azotobacter	955	58	12.6	626	2	Q3TS47_MOUSE	Q3ts47 mus musculu
883	58	12.6	175	2	Q5WAS8_BACSK	Q5was8 bacillus cl	956	58	12.6	629	2	Q86146_CAMJE	Q86146 campylobact
884	58	12.6	177	2	Q9EUW4_LISIN	Q9euw4 listeria in	957	58	12.6	662	2	Q3BQJ3_XANCS	Q3bj3 xanthomonas
885	58	12.6	185	2	Q5PJ65_SALPA	Q5pj65 salmonella	958	58	12.6	674	2	Q8PHZ1_XANAC	Q8phz1 xanthomonas
886	58	12.6	185	2	Q8ZK73_SALTY	Q8zk73 salmonella	959	58	12.6	675	2	Q2H4Y0_XANOR	Q2h4y0 xanthomonas
887	58	12.6	185	2	Q8Z152_SALTY	Q8z152 salmonella	960	58	12.6	675	2	Q5H226_XANOR	Q5h226 xanthomonas
888	58	12.6	186	2	Q9RYZ1_DEIRA	Q9ryz1 deinococcus	961	58	12.6	676	2	Q8XQP3_RALSO	Q8xqp3 ralstonia s
889	58	12.6	215	2	Q57NR2_SALCH	Q57nr2 salmonella	962	58	12.6	681	1	GAZL1_HUMAN	Q99501 homo sapien
890	58	12.6	215	2	Q5PCY5_SALPA	Q5pcy5 salmonella	963	58	12.6	681	2	Q4HU14_GIBZE	Q4hui4 gibberella
891	58	12.6	215	2	Q7CQF4_SALTY	Q7cqf4 salmonella	964	58	12.6	682	2	Q4HLX6_CAMLA	Q4hlx6 campylobact
892	58	12.6	215	2	Q8XF20_SALTY	Q8xf20 salmonella	965	58	12.6	695	2	Q6FJV9_CANGA	Q6fjv9 candida gla
893	58	12.6	232	2	Q5EQO0_VIBF1	Q5eqo0 vibrio fisc	966	58	12.6	743	2	Q9VQW0_DROME	Q9vqw0 drosophila
894	58	12.6	232	2	Q2LSR3_9DELT	Q2lsr3 syntrophus	967	58	12.6	758	2	Q51CV0_ENTHI	Q51cv0 entamoeba h
895	58	12.6	253	2	Q3PMW2_NITHA	Q3pmw2 nitrobacter	968	58	12.6	767	2	Q6OZP1_CAEBR	Q6ozp1 caenorhabdi
896	58	12.6	257	1	DPHB_METJA	Q58670 methanococ	969	58	12.6	778	2	Q37XW6_SPHAR	Q37xw6 novosphingo
897	58	12.6	263	2	Q9FP64_ORYSA	Q9fp64 oryza sativ	970	58	12.6	808	2	Q37XW6_SPHAR	Q37xw6 xenopus lae
898	58	12.6	264	2	Q33X14_9GAMM	Q33x14 shewanella	971	58	12.6	876	2	Q51593_XENIA	Q51593 aspergillus
899	58	12.6	277	1	RAFR_PEPDE	P43465 pediococcus	972	58	12.6	978	2	Q5BDP3_EMENI	Q5bdp3 arthroba
900	58	12.6	281	2	Q4B1K8_9URPK	Q4b1k8 polaronomas	973	58	12.6	1006	2	Q4NI49_9MICC	Q4nix0 desulfotale
901	58	12.6	283	2	Q37HA7_RHOPA	Q37ha7 rhodopseudo	974	58	12.6	1018	2	Q6ALX0_DESPS	Q6alx0 dechloromon
902	58	12.6	289	2	Q419J6_KINRA	Q419j6 kinococcus	975	58	12.6	1044	2	Q47D66_DECAR	Q47d66 dechloromon
903	58	12.6	314	2	Q6IK08_DROME	Q6ik08 drosophila	976	58	12.6	1051	2	Q5B9V4_EMENI	Q5b9v4 aspergillus
904	58	12.6	316	2	Q46SU8_RALEJ	Q46su8 ralstonia e	977	58	12.6	1056	2	Q7S8Q2_NEUCR	Q7s8q2 neurospora
905	58	12.6	322	2	Q3WKK7_9RHIZ	Q3wkk7 mesorhizobi	978	58	12.6	1056	2	Q3BS55_XANCS	Q3bs55 xanthomonas
906	58	12.6	325	2	Q9ELT9_9VIRU	Q9elt9 rice grassy	979	58	12.6	1056	2	Q8FJN1_XANAC	Q8fjn1 xanthomonas
907	58	12.6	326	2	Q2VR11_ANAPL	Q2vrl1 anas platyr	980	58	12.6	1109	2	Q7UR52_DROME	Q7ur52 drosophila

689	59	12.8	293	2	Q2ZX54_SHEPU	Q2zx54 shewanella	762	59	12.8	898	2	Q91592_XENLA	Q91592 xenopus lae
690	59	12.8	306	2	Q3GK95_FIRM	Q3gk95 syntrophomo	763	59	12.8	907	1	KCNB2_RAT	Q63099 rattus norv
691	59	12.8	310	2	Q37D92_RHOPA	Q37d92 rhodopseu	764	59	12.8	911	1	KCNB2_HUMAN	Q92953 homo sapien
692	59	12.8	310	2	Q9A410_CAUCR	Q9a410 caulobacter	765	59	12.8	911	1	KCNB2_RABIT	Q95111 oryctolagus
693	59	12.8	312	2	Q2J2C5_RHOPA	Q2j2c5 rhodopseu	766	59	12.8	911	2	Q7Z7D0_HUMAN	Q7z7d0 homo sapien
694	59	12.8	316	2	Q577P4_BRUAB	Q577p4 brucella ab	767	59	12.8	911	2	Q4ZHA6_BOVIN	Q4zha6 bos taurus
695	59	12.8	326	2	Q8FWG7_BRUSU	Q8fwg7 brucella su	768	59	12.8	936	2	Q6GNW5_XENLA	Q6gnw5 xenopus lae
696	59	12.8	326	2	Q8YBV7_BRUME	Q8ybv7 brucella me	769	59	12.8	971	2	Q5AXB1_ENEMI	Q5axb1 aspergillus
697	59	12.8	326	2	Q2YKB4_BRUA2	Q2ykb4 brucella ab	770	59	12.8	1027	2	Q488L9_COLP3	Q488l9 colwellia p
698	59	12.8	333	2	Q46SW4_RALEJ	Q46sw4 ralstonia e	771	59	12.8	1078	2	Q41S20_AZOVI	Q41s20 azotobacter
699	59	12.8	338	2	Q2VRR1_ANAPL	Q2vrr1 anas platyr	772	59	12.8	1211	2	Q57WZ8_9RYP	Q57wz8 trypanosoma
700	59	12.8	340	2	Q3M8T7_ANAVT	Q3m8t7 anabaena va	773	59	12.8	1463	2	Q4P3P5_USTMA	Q4p3p5 ustilago ma
701	59	12.8	345	1	ARC3_BACHK	Q6he28 bacillus th	774	58.5	12.7	126	2	Q36NM6_MARHY	Q36nm6 marinobacte
702	59	12.8	345	2	Q635F0_BACCZ	Q635f0 bacillus ce	775	58.5	12.7	133	2	Q8DA24_VIBVU	Q8da24 vibrio vuln
703	59	12.8	350	2	Q7MCV1_WOLUSU	Q7mcv1 wolinnella s	776	58.5	12.7	153	2	Q7MK55_VIBVU	Q7mk55 vibrio vuln
704	59	12.8	356	2	Q7XJY8_ORYSA	Q7xjy8 oryza sativ	777	58.5	12.7	156	2	Q3BQX7_XANCS	Q3bqx7 xanthomonas
705	59	12.8	361	2	Q46SQ0_RALEJ	Q46sq0 ralstonia e	778	58.5	12.7	161	2	Q3S1M0_CAEEL	Q3s1m0 caenorhabdi
706	59	12.8	363	2	Q3RU05_RALME	Q3ru05 ralstonia m	779	58.5	12.7	169	2	Q6MLM7_BDEBA	Q6mlm7 bdellovibri
707	59	12.8	369	2	Q7OZG4_GIALA	Q7ozg4 giardia lam	780	58.5	12.7	182	2	Q916C9_PSEAE	Q916c9 pseudomonas
708	59	12.8	370	2	Q98F86_RHILIO	Q98f86 rhizobium l	781	58.5	12.7	189	2	Q852L5_ORYSA	Q852l5 oryza sativ
709	59	12.8	377	2	Q4UM20_DESAC	Q4um20 desulfuromo	782	58.5	12.7	194	2	Q7QBB9_ANOXA	Q7qbb9 anopheles g
710	59	12.8	381	2	Q5OWF6_ENTHI	Q5owf6 entamoeba h	783	58.5	12.7	196	1	CLIPP_HELHP	Q7vin7 helicobacte
711	59	12.8	386	2	Q44OC5_SOLUS	Q44oc5 solibacter	784	58.5	12.7	200	2	Q4TT87_CAEEL	Q4tt87 caenorhabdi
712	59	12.8	419	2	Q97VB7_SULSO	Q97vb7 rhizobium s	785	58.5	12.7	215	2	Q2J2R0_RHOPA	Q2j2r0 rhodopseu
713	59	12.8	420	2	Q926F0_RHIME	Q926f0 rhizobium m	786	58.5	12.7	217	2	Q96XX6_SULTO	Q96xx6 sulfolobus
714	59	12.8	425	2	Q836T8_ENTPA	Q836t8 enterococcu	787	58.5	12.7	221	2	Q4SQX2_TETNG	Q4sqx2 tetraodon n
715	59	12.8	447	2	Q605T5_METCA	Q605t5 methylococc	788	58.5	12.7	222	2	Q7N7R7_PHOLL	Q7n7r7 photorhabdu
716	59	12.8	448	2	Q7NZNO_CHRVO	Q7nzn0 chromobacte	789	58.5	12.7	238	2	Q4SDB4_TETNG	Q4sdb4 tetraodon n
717	59	12.8	452	2	Q3BPW6_XANCS	Q3bpw6 xanthomonas	790	58.5	12.7	239	2	Q66IB5_BRARE	Q66ib5 brachydanio
718	59	12.8	463	2	Q6PC35_BRARE	Q6pc35 brachydanio	791	58.5	12.7	260	1	NRPN_HUMAN	Q60259 homo sapien
719	59	12.8	463	2	Q8JHG2_BRARE	Q8jhg2 brachydanio	792	58.5	12.7	260	2	Q81W69_HUMAN	Q81w69 homo sapien
720	59	12.8	479	1	NUON2_RHIME	P56911 rhizobium m	793	58.5	12.7	260	2	Q81W69_HUMAN	Q81w69 homo sapien
721	59	12.8	489	2	Q316W8_DESDG	Q316w8 desulfovibr	794	58.5	12.7	265	2	Q80Y16_LACPL	Q80yt6 lactobacill
722	59	12.8	490	2	Q2JPR9_9CYAN	Q2jpr9 cyanobacter	795	58.5	12.7	265	2	Q603A7_METCA	Q603a7 methylococc
723	59	12.8	502	2	Q2KU57_BORAV	Q2ku57 bordetella	796	58.5	12.7	268	2	Q3GQC6_9GAMM	Q3gqc6 psychrobact
724	59	12.8	526	2	Q6X1D5_9RHAB	Q6x1d5 aravan viru	797	58.5	12.7	277	2	Q3Y2T3_ENTFC	Q3y2t3 enterococcu
725	59	12.8	543	2	Q2T6B0_BURTH	Q2t6b0 burkholderi	798	58.5	12.7	299	2	Q7NWJ4_CHRVO	Q7nwj4 chromobacte
726	59	12.8	545	2	Q3HHA2_TRIER	Q3hha2 trichodesmi	799	58.5	12.7	299	2	Q7W0P0_BORPE	Q7w0p0 bordetella
727	59	12.8	552	2	Q41BY1_GIBZE	Q41by1 gibberella	800	58.5	12.7	299	2	Q7W3G6_BORPA	Q7w3g6 bordetella
728	59	12.8	557	2	Q5R7Q0_PONPY	Q5r7q0 pongo pygma	801	58.5	12.7	299	2	Q7WET6_BORPE	Q7wet6 bordetella
729	59	12.8	558	2	Q92C60_LISIN	Q92c60 listeria in	802	58.5	12.7	303	2	Q5XVK9_ARATH	Q5xvk9 arabidopsis
730	59	12.8	575	2	Q9QUU4_9MURI	Q9quu4 rattus sp.	803	58.5	12.7	321	1	TILS_BORPE	Q7vxt7 mesorhizobi
731	59	12.8	579	2	Q6U666_KLEPN	Q6u666 klebsiella	804	58.5	12.7	326	2	Q3WTT7_9RHIZ	Q3wtt7 psychrobact
732	59	12.8	598	2	Q4SURO_TETNG	Q4suro tetraodon n	805	58.5	12.7	328	2	Q6LEX6_PLAF7	Q6lex6 plasmodium
733	59	12.8	611	2	Q8WNQ3_PIG	Q8wnq3 sus scrofa	806	58.5	12.7	336	2	Q828R5_STRAM	Q828r5 streptomyce
734	59	12.8	623	2	Q53W46_THET8	Q53w46 thermus the	807	58.5	12.7	340	2	Q8R782_THETN	Q8r782 thermoanaer
735	59	12.8	653	2	Q5REB6_PONPY	Q5reb6 pongo pygma	808	58.5	12.7	341	2	Q3FBN1_9BURC	Q3fbn1 burkholderi
736	59	12.8	654	1	KCNM4_MOUSE	Q61423 mus musculu	809	58.5	12.7	344	2	Q4NG06_9MICC	Q4ng06 arthrobacte
737	59	12.8	654	2	KCNM4_MUSPF	Q28527 mustela put	810	58.5	12.7	347	2	Q47LN7_THEFY	Q47ln7 thermobifid
738	59	12.8	654	2	Q8CBF8_MOUSE	Q8cbf8 m 16 days n	811	58.5	12.7	351	2	Q3HBA5_TRIER	Q3hba5 trichodesmi
739	59	12.8	655	1	KCNM4_RAT	P15385 rattus norv	812	58.5	12.7	352	1	CCR5_CANPA	Q5ecr9 canis famil
740	59	12.8	660	1	KCNM4_BOVIN	P15385 rattus norv	813	58.5	12.7	356	2	Q44H85_CHRSL	Q44hs5 chromohalob
741	59	12.8	660	2	Q84MG6_ORYSA	Q84mg6 oryza sativ	814	58.5	12.7	359	2	Q5L5F2_CHLAB	Q5l5f2 chlamydophi
742	59	12.8	661	2	Q9GLF1_BOVIN	Q9glf1 bos taurus	815	58.5	12.7	366	2	Q9RRR9_BRAJA	Q9rrr9 bradyrhizob
743	59	12.8	662	2	Q9W336_COLL1	Q9w336 collumba liv	816	58.5	12.7	372	2	Q22K74_CALSA	Q22k74 caldicellul
744	59	12.8	662	2	Q9YX88_CHICK	Q9yx88 gallus gall	817	58.5	12.7	372	2	Q8SGX1_9SAUR	Q8sgx1 pareas macu
745	59	12.8	663	2	Q61VQ2_CAEER	Q61vq2 caenorhabdi	818	58.5	12.7	383	1	FAD6E_ARATH	Q8g3l3 arabidopsis
746	59	12.8	673	2	Q3WBA7_9ACTO	Q3wba7 frankia sp.	819	58.5	12.7	383	2	Q8LFZ8_ARATH	Q8lfz8 arabidopsis
747	59	12.8	677	2	Q388H5_9RYP	Q388h5 trypanosoma	820	58.5	12.7	384	2	Q8UAR7_AGR5	Q8uar7 agrobacteri
748	59	12.8	697	2	Q8JG57_XENLA	Q8jg57 xenopus lae	821	58.5	12.7	385	2	Q6ZLL9_ORYSA	Q6zll9 oryza sativ
749	59	12.8	700	2	Q5R4E7_PONPY	Q5r4e7 pongo pygma	822	58.5	12.7	389	2	Q7CS44_AGR5	Q7cs44 agrobacte
750	59	12.8	771	2	Q8OX33_MOUSE	Q8ox33 mus musculu	823	58.5	12.7	392	2	Q6C9T8_YARLI	Q6c9t8 yarrowia li
751	59	12.8	782	2	Q6LKY8_PHOPR	Q6lky8 photobacter	824	58.5	12.7	400	1	ERTU_HERAU	P42477 herpetosiph
752	59	12.8	787	2	Q5SMW7_ORYSA	Q5smw7 oryza sativ	825	58.5	12.7	409	2	Q8DBZ6_VIBVU	Q8dbz6 vibrio vuln
753	59	12.8	813	2	Q2NLD5_HUMAN	Q2nld5 homo sapien	826	58.5	12.7	411	2	Q9RU03_DEIRA	Q9ru03 deinococcus
754	59	12.8	816	2	Q98SV4_ICTPU	Q98sv4 ictalurus p	827	58.5	12.7	415	2	Q3CN28_ALTAT	Q3cn28 pseudolater
755	59	12.8	855	2	Q7NET0_MYCGA	Q7net0 mycoplasma	828	58.5	12.7	421	2	Q22600_9GAMM	Q22600 shewanella
756	59	12.8	857	1	KCNB1_MOUSE	Q03717 mus musculu	829	58.5	12.7	425	1	YOSB_SCHPO	Q9p7l2 schizosacch
757	59	12.8	857	1	KCNB1_RAT	P15387 rattus norv	830	58.5	12.7	425	2	Q3JF29_NITOC	Q3jf29 nitrosococc
758	59	12.8	857	2	Q8KOD1_MOUSE	Q8kod1 mus musculu	831	58.5	12.7	426	2	Q69513_MYCLE	Q69513 mycobacteri
759	59	12.8	858	1	KCNB1_HUMAN	Q14721 homo sapien	832	58.5	12.7	444	2	Q4D6T2_TYRC	Q4d6t2 trypanosoma
760	59	12.8	858	1	KCNB1_PIG	Q18968 sus scrofa	833	58.5	12.7	463	2	Q9CB73_MYCLE	Q9cb73 mycobacteri
761	59	12.8	858	1	KCNB1_RABIT	Q9mr19 oryctolagus	834	58.5	12.7	468	2	Q2STX5_BURTH	Q2stx5 burkholderi
										471	2	Q4S1G4_TETNG	Q4s1g4 tetraodon n

543	60	13.0	342	2	Q2L4T2_RAT	Q2L4t2 rattus norv	616	59.5	12.9	524	2	Q2YA78_NITMU	Q2ya78 nitrosospir
544	60	13.0	352	2	Q5DWS5_KARMI	Q5dws5 karlodinium	617	59.5	12.9	526	2	Q7VI06_HELHP	Q7vi06 helicobacte
545	60	13.0	365	2	Q69I35_EBVG	Q69i35 epstein-bar	618	59.5	12.9	527	1	TH11_TRYBB	Q06221 trypanosoma
546	60	13.0	369	2	Q6D4F3_ERWCT	Q6d4f3 erwinia car	619	59.5	12.9	527	1	Q26765_9TRYP	Q26765 trypanosoma
547	60	13.0	410	2	Q3VHD6_SPHPN	Q3vhd6 sphingopyxi	620	59.5	12.9	528	1	TH12_TRYBB	Q09037 trypanosoma
548	60	13.0	412	2	Q9I3M4_PSAE	Q9i3m4 pseudomonas	621	59.5	12.9	537	2	Q43S03_SOLUS	Q04303 solibacter
549	60	13.0	470	2	Q40AR9_9RHOB	Q40ar9 jannaschia	622	59.5	12.9	579	2	Q4EBF6_WLRCK	Q4ebf6 wolbachia e
550	60	13.0	497	1	LM22_EBV	Q40ar9 jannaschia	623	59.5	12.9	579	2	Q5GTF9_WLTR	Q5gtf9 wolbachia s
551	60	13.0	497	2	Q777H4_EBVG	P13285 epstein-bar	624	59.5	12.9	579	2	Q73I66_WOLPM	Q73i66 wolbachia p
552	60	13.0	502	2	Q9BGM9_9MAMM	Q777h4 epstein-bar	625	59.5	12.9	587	2	Q3HGA2_TRIER	Q3hga2 trichodesmi
553	60	13.0	518	2	Q9XB01_STRVG	Q9bgm9 tachyglouss	626	59.5	12.9	624	2	Q55X46_CRYNE	Q55x46 cryptococcu
554	60	13.0	519	2	Q82LQ9_STRAW	Q9xb01 streptomyce	627	59.5	12.9	624	2	Q5KMT6_CRYNE	Q5kmt6 cryptococcu
555	60	13.0	524	2	Q7T198_CHICK	Q82lq9 streptomyce	628	59.5	12.9	636	2	Q48GV9_PSE14	Q48gv9 pseudomonas
556	60	13.0	525	2	Q83J01_SHIFL	Q7t198 gallus gall	629	59.5	12.9	636	2	Q4ZR96_PSEU2	Q4zr96 pseudomonas
557	60	13.0	538	1	YIEC_ECOLI	Q83j01 shigella fl	630	59.5	12.9	636	2	Q87ZAB_PSESM	Q87zab pseudomonas
558	60	13.0	538	2	Q3YVL2_SHISS	P26318 escherichia	631	59.5	12.9	677	2	Q98TW3_XENLA	Q98tw3 xenopus lae
559	60	13.0	538	2	Q2M838_ECOLI	Q3yv12 shigella so	632	59.5	12.9	687	2	Q3H911_TRIER	Q3h911 trichodesmi
560	60	13.0	541	2	Q5KN13_CRYNE	Q2m838 escherichia	633	59.5	12.9	715	2	Q8PSH8_METMA	Q8ps8 methanosarc
561	60	13.0	565	2	Q8VD01_MOUSE	Q5kn13 cryptococcu	634	59.5	12.9	727	2	Q4ANX8_9CHLB	Q4anx8 chlorobium
562	60	13.0	580	2	Q7T195_CHICK	Q8vd01 mus musculu	635	59.5	12.9	735	2	Q5E3S0_VIRF1	Q5e3s0 vibrio fisc
563	60	13.0	605	2	Q7NHD8_GLOVI	Q7t195 gallus gall	636	59.5	12.9	752	2	Q3SFUA_THIDA	Q3sfua thiobacillu
564	60	13.0	611	2	Q8BYF6_MOUSE	Q7nhd8 gloeobacter	637	59.5	12.9	767	2	Q3G7T1_9DELT	Q3g7t1 pelobacter
565	60	13.0	616	2	Q581Z5_9TRYP	Q8byf6 m o day neo	638	59.5	12.9	768	2	Q4E426_TRYCR	Q4e426 trypanosoma
566	60	13.0	616	2	Q9Y1A2_TRYBB	Q581z5 trypanosoma	639	59.5	12.9	778	2	Q4RV23_TETNG	Q4rv23 tetraodon n
567	60	13.0	627	2	Q41RJ4_FERAC	Q9y1a2 trypanosoma	640	59.5	12.9	786	2	Q2IL98_9DELT	Q2il98 anaeromyxob
568	60	13.0	655	2	Q3MWI3_9ACTO	Q41rj4 ferroplasma	641	59.5	12.9	841	2	Q8H105_ARATH	Q8h105 arabidopsis
569	60	13.0	738	2	Q3JDI8_NITOC	Q3mw13 frankia sp.	642	59.5	12.9	847	2	Q8RWY4_ARATH	Q8rwy4 arabidopsis
570	60	13.0	756	2	Q55Z68_CRYNE	Q3jd18 nitrococcu	643	59.5	12.9	894	2	Q9SGW2_ARATH	Q9sgw2 arabidopsis
571	60	13.0	793	2	Q94BY0_ARATH	Q55z68 cryptococcu	644	59.5	12.9	940	2	Q8T043_DROME	Q8t043 drosophila
572	60	13.0	801	2	Q4A0U1_9BURK	Q94by0 arabidopsis	645	59.5	12.9	996	2	Q2XM19_PSEPU	Q2xm19 pseudomonas
573	60	13.0	819	1	US6NL_MOUSE	Q4a0u1 polaromonas	646	59.5	12.9	1037	2	Q9VZ53_DROME	Q9vz53 drosophila
574	60	13.0	819	2	Q3U2W3_MOUSE	Q80xc3 mus musculu	647	59.5	12.9	1082	2	Q43L65_SOLUS	Q43l65 solibacter
575	60	13.0	850	2	Q2MHK9_BRARE	Q3u2w3 mus musculu	648	59.5	12.9	1138	2	Q43L65_SOLUS	Q43l65 solibacter
576	60	13.0	876	2	Q4ITTS_AZOVI	Q2mhk9 brachydanio	649	59.5	12.9	1326	2	Q4DLK6_TRYCR	Q4dlk6 trypanosoma
577	60	13.0	1056	2	Q4UVM2_XANC8	Q4itts azotobacter	650	59.5	12.9	1800	2	Q54PV1_DICDI	Q54pv1 dictyosteli
578	60	13.0	1056	2	Q8P875_XANCP	Q4uvw2 xanthomonas	651	59.5	12.9	1800	2	Q8I7P5_DICDI	Q8i7p5 dictyosteli
579	60	13.0	1157	2	Q6BRA0_DEBHA	Q8p875 xanthomonas	652	59.5	12.9	119	2	Q9GMZ2_PIG	Q9gmz2 sus scrofa
580	60	13.0	3187	2	Q4SER6_TETNG	Q6bra0 debaryomyce	653	59	12.8	119	2	Q8XBD2_ECO57	Q8xbd2 escherichia
581	60	13.0	4149	2	Q4AC22_CHLRE	Q4ser6 tetraodon n	654	59	12.8	130	2	Q41BF4_EC057	Q41bf4 esguibacte
582	60	13.0	5218	1	HTS1_COCOA	Q4ac22 chlamydomon	655	59	12.8	137	2	Q3GDC8_9FIRM	Q3gdc8 syntrophomo
583	59.5	12.9	186	2	Q2U0X4_ASPOR	Q2u0x4 aspergillus	656	59	12.8	149	2	Q88UG2_LACPL	Q88ug2 lactobacill
584	59.5	12.9	209	2	Q5KN00_CRYNE	Q5kn00 cryptococcu	657	59	12.8	149	2	Q88UG2_LACPL	Q88ug2 lactobacill
585	59.5	12.9	214	2	Q7N459_PHOLL	Q7n459 photorhabdu	658	59	12.8	150	2	Q6D7R0_ERWCT	Q6d7r0 erwinia car
586	59.5	12.9	216	2	Q9GJG8_SALTR	Q9gjg8 salmo trutt	659	59	12.8	155	2	Q923L7_MOUSE	Q923l7 mus musculu
587	59.5	12.9	216	2	Q9GJG9_SALTR	Q9gjg9 salmo trutt	660	59	12.8	165	2	Q3QSP5_9RHOB	Q3qsp5 silicibacte
588	59.5	12.9	216	2	Q9GJH0_SALTR	Q9gjh0 salmo trutt	661	59	12.8	167	2	Q8W9B3_VOMUR	Q8w9b3 vombatus ur
589	59.5	12.9	217	2	Q9GJH3_SALTR	Q9gjh3 salmo trutt	662	59	12.8	169	2	Q744R5_MYCPA	Q744r5 mycobacteri
590	59.5	12.9	217	2	Q9GJH4_SALTR	Q9gjh4 salmo trutt	663	59	12.8	177	2	Q92713_FALPE	Q92713 falco pereg
591	59.5	12.9	217	2	Q9GJH6_SALTR	Q9gjh6 salmo trutt	664	59	12.8	177	2	Q92AM4_LISIN	Q92am4 listeria in
592	59.5	12.9	217	2	Q9GJH7_SALTR	Q9gjh7 salmo trutt	665	59	12.8	189	2	Q6X9K8_SULIS	Q6x9k8 sulfolobus
593	59.5	12.9	223	2	Q6PER5_MOUSE	Q9gjh7 salmo trutt	666	59	12.8	189	2	Q6X9L0_SULIS	Q6x9l0 sulfolobus
594	59.5	12.9	228	2	Q3PPC1_NITHA	Q6per5 mus musculu	667	59	12.8	189	2	Q6X9L1_SULIS	Q6x9l1 sulfolobus
595	59.5	12.9	228	2	Q4RQJ4_TETNG	Q3ppc1 nitrobacter	668	59	12.8	189	2	Q6X9L7_SULIS	Q6x9l7 sulfolobus
596	59.5	12.9	260	2	Q86AQ7_DICDI	Q4rjq4 tetraodon n	669	59	12.8	189	2	Q6X9M0_SULIS	Q6x9m0 sulfolobus
597	59.5	12.9	267	2	Q9CG47_LACLA	Q86aq7 dictyosteli	670	59	12.8	189	2	Q3WSP0_9RHIZ	Q3wsp0 mesorhizobi
598	59.5	12.9	298	2	Q9KKR2_VIBCH	Q9cg47 lactococcus	671	59	12.8	215	1	YCHE_ECOLI	Q25743 escherichia
599	59.5	12.9	341	2	Q880A3_PSESM	Q9kk2 vibrio chol	672	59	12.8	215	2	Q31ZT2_SHIBS	Q31zt2 shigella bo
600	59.5	12.9	342	2	Q9G5Z0_9SAUR	Q880a3 pseudomonas	673	59	12.8	215	2	Q320V6_SHISS	Q320v6 shigella so
601	59.5	12.9	348	2	Q8XKM0_CLOPE	Q9g5z0 pseudocalot	674	59	12.8	215	2	Q398G3_BURS3	Q398g3 burkholderi
602	59.5	12.9	350	2	Q3E0B4_CHLAU	Q8xkm0 clostridium	675	59	12.8	215	2	Q8FHX1_ECOL6	Q8fmx1 escherichia
603	59.5	12.9	356	2	Q3YMM0_NPVLD	Q3e0b4 chloroflexu	676	59	12.8	215	2	Q8JRN1_SHIFL	Q8jrn1 shigella fl
604	59.5	12.9	384	2	Q72DS9_DESVH	Q3ymm0 lymantria d	677	59	12.8	215	2	Q8XDA5_EC057	Q8xda5 escherichia
605	59.5	12.9	385	2	Q4SSP1_TETNG	Q72ds9 desulfovibr	678	59	12.8	231	2	Q2Z5B0_9GAMM	Q2z5b0 shewanella
606	59.5	12.9	396	2	Q9U3R3_CAEEL	Q4ssp1 tetraodon n	679	59	12.8	231	2	Q360K8_9GAMM	Q360k8 shewanella
607	59.5	12.9	397	2	Q8XSK5_RALSO	Q9u3r3 caenorhabdi	680	59	12.8	255	2	Q36DZ6_9GAMM	Q36dz6 burkholderi
608	59.5	12.9	411	2	Q35ES6_BRAD	Q8xsk5 ralstonia s	681	59	12.8	262	2	Q3FB45_9BURK	Q3fb45 burkholderi
609	59.5	12.9	421	2	Q2ZU62_SHEPU	Q35es6 bradyrhizob	682	59	12.8	262	2	Q4XRU0_9PROT	Q4xru0 magnetococc
610	59.5	12.9	426	2	Q6FJK9_CANGA	Q2zu62 shewanella	683	59	12.8	276	2	Q47F87_DECAR	Q47f87 dechloromon
611	59.5	12.9	431	2	Q7XTD3_ORYGA	Q6fjk9 candida gla	684	59	12.8	284	2	Q594H3_9SPHN	Q594h3 agrobacteri
612	59.5	12.9	459	2	Q3GU76_9ACTO	Q7xtd3 oryza sativ	685	59	12.8	293	1	PUR7_BORBR	Q7wm11 bordetella
613	59.5	12.9	467	2	Q2LVB0_9DELT	Q3gu76 nocardioide	686	59	12.8	293	1	PUR7_BORPA	Q7wb15 bordetella
614	59.5	12.9	467	2	Q2KYV5_BORAV	Q2lvb0 syntrophus	687	59	12.8	293	1	PUR7_BORPE	Q7vy42 bordetella
615	59.5	12.9	481	2	Q4E742_9RICK	Q2kyv5 bordetella	688	59	12.8	293	2	Q2X418_9GAMM	Q2x418 shewanella

397	61	13.2	438	2	Q3AW34_SYNS9	Q3aw34	synchococc	470	60.5	13.1	558	2	Q7V8R1_PROMM	Q7v8r1	prochloroco
398	61	13.2	447	2	Q37Q12_SPHAR	Q37q12	novosphingo	471	60.5	13.1	685	2	Q2WWT4_9GAMM	Q2wwt4	shewanella
399	61	13.2	452	2	Q2P0F6_XANOR	Q2p0f6	xanthomonas	472	60.5	13.1	685	2	Q2Z423_9GAMM	Q2z423	shewanella
400	61	13.2	461	2	Q7ACQ0_ECO57	Q7acq0	escherichia	473	60.5	13.1	685	2	Q2ZP33_SHEPU	Q2zp33	shewanella
401	61	13.2	461	2	Q9S5F6_ECOLI	Q9s5f6	escherichia	474	60.5	13.1	685	2	Q35TT5_9GAMM	Q35tt5	shewanella
402	61	13.2	463	2	Q59471_PYROH	Q59471	pyrococcus	475	60.5	13.1	726	2	Q4HSU4_CAMUP	Q4hsu4	campylobact
403	61	13.2	463	2	Q9V1R1_PYRAB	Q9v1r1	pyrococcus	476	60.5	13.1	728	1	PURL_CAMJE	Q9huk4	campylobact
404	61	13.2	463	2	Q85337_ECOLI	Q85337	escherichia	477	60.5	13.1	728	1	PURL_CAMJR	Q5huk4	campylobact
405	61	13.2	463	2	Q7DBP7_ECO57	Q7dbf2	escherichia	478	60.5	13.1	728	2	Q4HIH9_CAMCO	Q4hih9	campylobact
406	61	13.2	484	2	Q5GXAI_XANOR	Q5gxai	xanthomonas	479	60.5	13.1	742	2	Q9Q0S7_9NFA	Q9q0s7	influenza a
407	61	13.2	488	2	Q5Z1J6_NOCFA	Q5z1j6	nocardia fa	480	60.5	13.1	776	2	Q7NT42_CHRVO	Q7nt42	chromobacte
408	61	13.2	502	2	Q5DAP6_SCHJA	Q5dap6	schistosoma	481	60.5	13.1	786	2	Q2S1W1_9SPHI	Q2s1w1	salinibacte
409	61	13.2	520	2	Q9SHZ3_ARATH	Q9shz3	arabidopsis	482	60.5	13.1	878	2	Q35UA3_9GAMM	Q35ua3	shewanella
410	61	13.2	542	2	Q5YVG0_NOCFA	Q5yvg0	nocardia fa	483	60.5	13.1	917	2	Q75V17_STAWA	Q75v17	staphylococ
411	61	13.2	568	2	Q61FR3_CABBR	Q61fr3	caenorhabdi	484	60.5	13.1	1038	2	Q7PPM7_ANOGA	Q7ppm7	anopheles g
412	61	13.2	570	2	Q386Y4_TRYPTP	Q386y4	trypanosoma	485	60.5	13.1	1155	2	Q4IU17_AGOVI	Q4iu17	azotobacter
413	61	13.2	638	2	Q6MLY6_DBEBA	Q6mly6	bellovobiri	486	60.5	13.1	1227	2	Q2SGU1_9GAMM	Q2sgu1	hahella che
414	61	13.2	651	2	Q9DDN7_9TELE	Q9ddn7	apteronotus	487	60.5	13.1	1285	2	Q2PWA0_9REOV	Q2pwa0	avian ortho
415	61	13.2	653	2	Q73TB8_MYCPA	Q73tb8	mycobacteri	488	60.5	13.1	1285	2	Q5IS12_9REOV	Q5is12	avian ortho
416	61	13.2	742	2	Q2WNE2_CLOBE	Q2wne2	clostridium	489	60.5	13.1	1285	2	Q5IS13_9REOV	Q5is13	avian ortho
417	61	13.2	874	2	Q33T29_9GAMM	Q33t29	shewanella	490	60.5	13.1	1285	2	Q5IS14_9REOV	Q5is14	avian ortho
418	61	13.2	1069	2	Q3P712_PARCOCU	Q3p712	paracoccus	491	60.5	13.1	1285	2	Q5IS15_9REOV	Q5is15	avian ortho
419	61	13.2	1305	1	TCGAP_MOUSE	Q80yfg9	mus musculus	492	60.5	13.1	1285	2	Q5IS16_9REOV	Q5is16	avian ortho
420	61	13.2	1324	2	Q3UQS4_MOUSE	Q3uqs4	mus musculus	493	60.5	13.1	1285	2	Q5IS17_9REOV	Q5is17	avian ortho
421	61	13.2	1526	2	Q5K7V4_CRYNE	Q5k7v4	cryptococcu	494	60.5	13.1	1285	2	Q5IS18_9REOV	Q5is18	avian ortho
422	61	13.2	1866	2	Q55IB7_CRYNE	Q55ib7	cryptococcu	495	60.5	13.1	1285	2	Q5IS19_9REOV	Q5is19	avian ortho
423	60.5	13.1	86	2	Q8ZHN5_STRAW	Q8zhn5	streptomyce	496	60.5	13.1	1285	2	Q8JUW1_9REOV	Q8juw1	avian reovi
424	60.5	13.1	146	2	Q3FHO1_9BURK	Q3fho1	burkholderi	497	60.5	13.1	1319	2	Q5AYC8_ENENI	Q5ayc8	aspergillus
425	60.5	13.1	163	2	Q5GYF6_XANOR	Q5gyf6	xanthomonas	498	60.5	13.1	1748	2	Q9HGZ5_ASPOR	Q9hgz5	aspergillus
426	60.5	13.1	165	2	Q3E5X3_CHLAU	Q3e5x3	chloroflexu	499	60	13.0	71	1	VITB1_XENLA	P19010	xenopus lae
427	60.5	13.1	166	2	Q2P1G0_XANOR	Q2p1g0	xanthomonas	500	60	13.0	165	2	Q8EPX3_OCEIH	Q8epx3	oceanobacil
428	60.5	13.1	176	2	Q9VUP1_DROME	Q9vup1	drosophila	501	60	13.0	196	2	Q2VL37_9PRJM	Q2vl37	eulemur ful
429	60.5	13.1	210	1	PYRE_BACAN	Q81wf6	bacillus an	502	60	13.0	208	2	Q2VL38_OTOGA	Q2vl38	otolemur ga
430	60.5	13.1	210	1	PYRE_BACCI	Q73217	bacillus ce	503	60	13.0	208	2	Q2VL39_PITPI	Q2vl39	pithecia pi
431	60.5	13.1	210	1	PYRE_BACCR	Q819e7	bacillus th	504	60	13.0	208	2	Q2VL40_LAGLA	Q2vl40	lagothrix l
432	60.5	13.1	210	1	PYRE_BACHK	Q6het2	bacillus th	505	60	13.0	208	2	Q2VL41_ATEGE	Q2vl41	ateles geof
433	60.5	13.1	210	1	Q4MJ46_BACCE	Q4mj46	bacillus ce	506	60	13.0	208	2	Q2VL42_COLAN	Q2vl42	colobus ang
434	60.5	13.1	227	2	Q8EX00_ARATH	Q8ex00	arabidopsis	507	60	13.0	208	2	Q2VL43_CERCP	Q2vl43	cercopithe
435	60.5	13.1	241	2	Q3SSH3_NITWN	Q3ssh3	nitrobacter	508	60	13.0	208	2	Q2VL44_PAPAN	Q2vl44	papio anubi
436	60.5	13.1	253	2	Q3QPP6_ALTAT	Q3qpp6	pseudocalt	509	60	13.0	208	2	Q2VL45_MANLE	Q2vl45	mandrillus
437	60.5	13.1	279	2	Q3CPE6_PLATE	Q6w741	pediculus h	510	60	13.0	208	2	Q2VL46_HYLSY	Q2vl46	hylobates s
438	60.5	13.1	286	2	Q417D8_KINRA	Q417d8	kineococcus	511	60	13.0	208	2	Q2VL47_PONPA	Q2vl47	pongo pygma
439	60.5	13.1	289	2	Q7S921_NEUCR	Q7s921	neurospora	512	60	13.0	208	2	Q2VL48_GORGO	Q2vl48	gorilla gor
440	60.5	13.1	295	2	Q22885_ARATH	Q22885	arabidopsis	513	60	13.0	208	2	Q2VL49_PANPA	Q2vl49	pan paniscu
441	60.5	13.1	306	2	Q21PE9_9DELT	Q21pe9	anaeromyxob	514	60	13.0	218	2	Q6LT63_PROPR	Q6lt63	photobacter
442	60.5	13.1	312	2	Q9KEQ5_BACBE	Q9keq5	bacillus ha	515	60	13.0	249	2	Q8WM93_BRARE	Q8wm93	brachydantlo
443	60.5	13.1	319	2	Q4YCE8_PLABE	Q4yce8	plasmodium	516	60	13.0	257	2	Q3KXP8_XENLA	Q3kxp8	xenopus lae
444	60.5	13.1	326	2	Q9Y7W6_SULSO	Q9y7w6	sulfolobus	517	60	13.0	275	2	Q9VLF8_DROME	Q9vlf8	drosophila
445	60.5	13.1	327	2	Q5XWR0_SOLTU	Q5xwr0	solanum tub	518	60	13.0	277	2	Q4AYA9_9BURK	Q4aya9	polaromonas
446	60.5	13.1	336	2	Q2OCE0_MEGAN	Q2qce0	megadyptes	519	60	13.0	283	2	Q42AB6_DESHA	Q42ab6	desulfitoba
447	60.5	13.1	340	2	Q8LAZ5_ARATH	Q8laz5	arabidopsis	520	60	13.0	288	2	Q88IQ0_PSEPK	Q88iq0	pseudomonas
448	60.5	13.1	354	2	Q9M9T5_ARATH	Q9m9t5	arabidopsis	521	60	13.0	316	2	Q9VWN1_DROME	Q9vwn1	drosophila
449	60.5	13.1	359	2	Q3XNW7_9PROT	Q3xmw7	magnetococc	522	60	13.0	318	2	Q351J2_9GAMM	Q351j2	alkalilimni
450	60.5	13.1	416	2	Q33NX9_9GAMM	Q33nx9	shewanella	523	60	13.0	324	2	Q986J3_RHILO	Q986j3	rhizobium l
451	60.5	13.1	416	2	Q3NX34_9GAMM	Q3nx34	shewanella	524	60	13.0	325	2	Q986J3_RHILO	Q986j3	rhizobium l
452	60.5	13.1	427	2	Q9A315_CAUCR	Q9a315	caulobacter	525	60	13.0	325	2	Q7XMF8_ORYSA	Q7xmf8	oryza sativ
453	60.5	13.1	434	2	Q4MG72_BACCE	Q4mg72	bacillus ce	526	60	13.0	341	1	PAX9_CALGO	Q2vl59	callinico g
454	60.5	13.1	434	2	Q63AK9_BACCC	Q63ak9	bacillus ce	527	60	13.0	341	1	PAX9_CALJA	Q2vl58	callithrix
455	60.5	13.1	434	2	Q81CL5_BACCR	Q81cl5	bacillus ce	528	60	13.0	341	1	PAX9_DAUMA	Q2vl53	daubentonia
456	60.5	13.1	463	2	Q8D167_YERSINIA PE	Q8d167	yersinia pe	529	60	13.0	341	1	PAX9_HUMAN	P55771	homo sapien
457	60.5	13.1	463	2	Q66DX2_YERPS	Q66dx2	yersinia ps	530	60	13.0	341	1	PAX9_LEMCA	Q2vl52	lemur catia
458	60.5	13.1	463	2	Q8ZC25_YERPE	Q8zc25	yersinia pe	531	60	13.0	341	1	PAX9_LEORO	Q2vl57	leontopithe
459	60.5	13.1	474	2	Q3JUI22_BURP1	Q3jiz2	burkholderi	532	60	13.0	341	1	PAX9_LEPPD	Q2vl51	lepilemur e
460	60.5	13.1	474	2	Q63187_BURPDS	Q63187	burkholderi	533	60	13.0	341	1	PAX9_MACWD	Q2vl61	macaca mula
461	60.5	13.1	478	2	Q86BK5_DROME	Q86bk5	drosophila	534	60	13.0	341	1	PAX9_PANTR	Q2vl62	pan troglod
462	60.5	13.1	484	2	Q4ZBP3_9VIRU	Q4zbp3	bacterioph	535	60	13.0	341	1	PAX9_PERPO	Q2vl54	perodicticu
463	60.5	13.1	484	2	Q4ZDK0_9CAUD	Q4zdk0	bacterioph	536	60	13.0	341	1	PAX9_PROVC	Q2vl50	propithecus
464	60.5	13.1	484	2	Q6R861_9CAUD	Q6r861	bacterioph	537	60	13.0	341	1	PAX9_SAIIBB	Q2vl60	saimiri bol
465	60.5	13.1	516	2	Q9M174_ARATH	Q9m174	arabidopsis	538	60	13.0	341	2	Q2L4T1_HUMAN	Q2l4t1	homo sapien
466	60.5	13.1	547	2	Q4R401_MACFA	Q4r401	macaca fasc	539	60	13.0	341	2	Q2VL55_TARSY	Q2vl55	tarsius syr
467	60.5	13.1	560	2	Q5P1A5_AZOSE	Q5p1a5	azocarcus sp	540	60	13.0	342	1	PAX9_MOUSE	P47242	mus musculu
468	60.5	13.1	618	2	Q9GGM9_9POAL	Q9ggm9	carex backi	541	60	13.0	342	2	Q3V1K1_MOUSE	Q3v1k1	mus musculu
469	60.5	13.1	638	1	KCNC2_RAT	P22462	rattus norv	542	60	13.0	342	2	Q8BS81_MOUSE	Q8bs81	mus musculu

251	62.5	13.6	504	2	Q7S9U0_NEUCR	Q7S9U0_neurospora	324	61.5	13.3	321	2	Q44JU7_CHRSL	Q44ju7 chromohalob
252	62.5	13.6	525	2	Q9NCZ9_TRYCO	Q9ncz9 trypanosoma	325	61.5	13.3	324	2	Q3H547_7ACTO	Q3h547 nocardioide
253	62.5	13.6	525	2	Q76235_TRYCO	Q76235 trypanosoma	326	61.5	13.3	327	2	Q6MJX9_DEBEA	Q6mjx9 bdellovibri
254	62.5	13.6	539	2	Q9RD59_STRCO	Q9rd59 streptomyce	327	61.5	13.3	339	1	TM66_FONPY	Q5r491 pongo pygma
255	62.5	13.6	552	2	Q33287_SHEWANA	Q33287 shewanella	328	61.5	13.3	342	1	IS1A_SYNY3	Q55274 rhodospirill
256	62.5	13.6	557	2	Q7XQW8_ORYZA	Q7xqw8 oryza sativ	329	61.5	13.3	345	2	Q2RST8_RHORU	Q2rst8 rhodospirill
257	62.5	13.6	580	2	Q5T6S3_HUMAN	Q5t6s3 homo sapien	330	61.5	13.3	342	2	Q6R122_MOUSE	Q6r122 mus musculu
258	62.5	13.6	604	2	Q9VNP7_DROME	Q9vnp7 drosophila	331	61.5	13.3	347	2	Q88VV9_LACPL	Q88vv9 lactobacill
259	62.5	13.6	621	2	Q6N038_HUMAN	Q6n038 homo sapien	332	61.5	13.3	381	2	Q4Q9N5_LEIMA	Q4q9n5 leishmania
260	62.5	13.6	663	2	Q72PX8_LEPIC	Q72px8 leptospira	333	61.5	13.3	382	2	Q89MV3_BRADA	Q89mv3 bradyrhizob
261	62.5	13.6	663	2	Q8F6A7_LEPIC	Q8f6a7 leptospira	334	61.5	13.3	399	2	Q340Q9_RHOPE	Q340q9 rhodopseudo
262	62.5	13.6	670	2	Q4SQ15_TETNG	Q4sq15 tetraodon n	335	61.5	13.3	411	2	Q5WKBS_BACSK	Q5wkb5 bacillus cl
263	62.5	13.6	685	2	Q8EEJ6_SHEON	Q8eej6 shewanella	336	61.5	13.3	427	2	Q487R5_COLP3	Q487r5 colwellia p
264	62.5	13.6	700	2	Q8TG00_ASPFU	Q8tg00 aspergillus	337	61.5	13.3	430	2	Q9TS97_CHLPN	Q9ts97 chlamydia p
265	62.5	13.6	760	2	Q7XNU5_ORYZA	Q7xnu5 oryza sativ	338	61.5	13.3	433	2	Q9KL77_CHLPN	Q9kl77 chlamydia p
266	62.5	13.6	769	1	KCN3_MOUSE	Q63959 mus musculu	339	61.5	13.3	433	2	Q9Z748_CHLPN	Q9z748 chlamydia p
267	62.5	13.6	850	2	Q6SMA9_BACLD	Q6sma9 bacillus li	340	61.5	13.3	434	2	Q736Y4_BACCL	Q736y4 bacillus ce
268	62.5	13.6	910	1	SYL_NEIMA	Q9jw39 neisseria m	341	61.5	13.3	437	2	Q8NF56_HUMAN	Q8nf56 homo sapien
269	62.5	13.6	1048	1	SILA_SALTY	Q9zhe9 salmonella	342	61.5	13.3	445	2	Q57I33_SALCH	Q57i33 salmonella
270	62.5	13.6	1048	2	Q2ZSNO_SHEPU	Q2zsn0 shewanella	343	61.5	13.3	445	2	Q5PKR4_SALPA	Q5pkr4 salmonella
271	62.5	13.6	1048	2	Q3G640_9GAMM	Q3g640 shewanella	344	61.5	13.3	445	2	Q8ZL09_SALTY	Q8ztl09 salmonella
272	62.5	13.6	1048	2	Q6MXQ0_SERMA	Q6mxq0 serratia ma	345	61.5	13.3	445	2	Q8Z2L3_SALTI	Q8z2l3 salmonella
273	62.5	13.6	1487	2	Q3NTP0_SHEFR	Q3ntp0 shewanella	346	61.5	13.3	458	2	Q6D860_ERMCT	Q6d860 erwinia car
274	62.5	13.6	1489	2	Q2J1T7_RHOPE	Q2j1t7 rhodopseudo	347	61.5	13.3	461	2	Q4FFN8_9ILIL	Q4ffn8 acorus amer
275	62	13.4	150	2	Q893N4_CLOTE	Q893n4 clostridium	348	61.5	13.3	493	2	Q4CX55_TRYCR	Q4cx55 trypanosoma
276	62	13.4	179	1	DSBB_HEDU	Q7vxy2 haemophilus	349	61.5	13.3	495	2	Q4SR06_TETNG	Q4srq6 tetraodon n
277	62	13.4	189	2	Q6X9L3_SULIS	Q6x9l3 sulfolobus	350	61.5	13.3	522	2	Q84DU5_LISIV	Q84du5 listeria iv
278	62	13.4	241	2	Q3GLJ7_9DELT	Q3glj7 pelobacter	351	61.5	13.3	523	2	Q84DU4_LISIV	Q84du4 listeria iv
279	62	13.4	269	2	Q6YVW5_ORYZA	Q6yvw5 oryza sativ	352	61.5	13.3	524	1	P60_LISIV	Q9qew6 measles vir
280	62	13.4	287	2	Q3KR82_RAT	Q3kr82 rattus norv	353	61.5	13.3	545	2	Q9QW66_9PARA	Q9qwu6 drosophila
281	62	13.4	297	2	Q3BQX5_XANC5	Q3bx5 xanthomonas	354	61.5	13.3	549	2	Q9V3U6_DROME	Q9v3u6 drosophila
282	62	13.4	308	2	Q6L8X8_CAEBR	Q6l8x8 caenorhabdi	355	61.5	13.3	566	2	Q73L70_TREDE	Q73l70 treponema d
283	62	13.4	308	2	Q8BFU1_MOUSE	Q8bfu1 m 7 days ne	356	61.5	13.3	592	2	Q9PVDI_XENLA	Q9pvd1 xenopus lae
284	62	13.4	381	2	Q8UC07_AGRT5	Q8uc07 agrobacteri	357	61.5	13.3	637	2	Q36LA4_MARHY	Q36la4 marinobacte
285	62	13.4	393	2	Q7CWG7_AGRT5	Q7cwg7 agrobacteri	358	61.5	13.3	668	1	RN139_MOUSE	Q7tmv1 mus musculu
286	62	13.4	414	2	Q32383_STRGR	Q32383 streptomyce	359	61.5	13.3	701	2	Q4G0I9_HUMAN	Q4g0i9 homo sapien
287	62	13.4	416	2	Q3QHT7_9GAMM	Q3qht7 shewanella	360	61.5	13.3	805	2	Q6ZL28_BURMA	Q6zl28 burkholderi
288	62	13.4	417	2	Q3IGF3_PSEHT	Q3igf3 pseudoealter	361	61.5	13.3	807	2	Q3JTE4_BURPI	Q3jte4 burkholderi
289	62	13.4	419	2	Q7XTD2_ORYZA	Q7xtcd2 oryza sativ	362	61.5	13.3	831	2	Q60XB5_CAEBR	Q60xb5 caenorhabdi
290	62	13.4	445	2	Q96X94_SULTO	Q96x94 sulfolobus	363	61.5	13.3	854	2	Q4DIM4_TRYCR	Q4dim4 trypanosoma
291	62	13.4	445	2	Q2R394_ORYZA	Q2r394 oryza sativ	364	61.5	13.3	855	2	Q63TB1_BURPS	Q63tb1 burkholderi
292	62	13.4	470	2	Q8PHB1_XANAC	Q8phb1 xanthomonas	365	61.5	13.3	913	2	Q2KGW0_MAGGR	Q2kgw0 magnaporthe
293	62	13.4	489	2	Q6SUC0_MANSM	Q6suc0 manheimia	366	61.5	13.3	977	1	FCRL5_HUMAN	Q96rd9 homo sapien
294	62	13.4	526	2	Q2LOP8_BORAV	Q2lop8 bordetella	367	61.5	13.3	990	2	Q32MR1_HUMAN	Q32mr1 homo sapien
295	62	13.4	558	2	Q8NIV9_HUMAN	Q8niv9 homo sapien	368	61.5	13.3	990	2	Q6Q4G3_HUMAN	Q6q4g3 homo sapien
296	62	13.4	568	2	Q2JR78_9CYAN	Q2jr78 cyanobacter	369	61.5	13.3	998	2	Q495Q3_HUMAN	Q495q3 homo sapien
297	62	13.4	577	2	Q9V7C4_DROME	Q9v7c4 drosophila	370	61.5	13.3	1145	2	Q8GUE7_9ILIL	Q8gue7 cymodocea n
298	62	13.4	581	1	FUR4_SCHPO	Q10279 schizosacch	371	61.5	13.3	1322	2	Q5AL53_CANAL	Q5al53 candida alb
299	62	13.4	613	2	Q96PR0_HUMAN	Q96pr0 homo sapien	372	61.5	13.3	1499	2	Q8YK83_ANASP	Q8yk83 anabaena sp
300	62	13.4	629	2	Q86W09_HUMAN	Q86w09 homo sapien	373	61	13.2	100	2	Q6VE83_PSESY	Q6ve83 pseudomonas
301	62	13.4	638	2	Q96PR1_HUMAN	Q96pr1 homo sapien	374	61	13.2	112	2	Q2K4H0_RHET	Q2k4h0 rhizobium e
302	62	13.4	641	2	Q4LE77_HUMAN	Q4le77 homo sapien	375	61	13.2	139	2	Q87HL7_VIBPA	Q87hl7 vibrio para
303	62	13.4	777	2	Q51502_PSEAE	Q51502 pseudomonas	376	61	13.2	157	2	Q8DV17_STRMU	Q8dv17 streptococc
304	62	13.4	862	2	Q6MYC9_ASPFU	Q6myc9 aspergillus	377	61	13.2	173	2	Q7Q505_ANOGA	Q7q505 anopheles g
305	62	13.4	962	2	Q6BZ68_DEBHA	Q6bz68 debaryomyce	378	61	13.2	173	2	Q6MY22_SERMA	Q6my22 serratia ma
306	62	13.4	1025	2	Q4QGS8_LEIMA	Q4qgs8 leishmania	379	61	13.2	180	2	Q81IG5_MOUSE	Q81ig6 mus musculu
307	62	13.4	1057	2	Q6FTI2_CANGA	Q6fti2 candida gla	380	61	13.2	187	2	Q8SHU1_XENTR	Q8shu1 xenopus tro
308	62	13.4	2325	1	SDK_CABEL	Q9n3x8 caenorhabdi	381	61	13.2	198	2	Q379H1_RHOPE	Q379h1 rhodopseudo
309	61.5	13.3	99	2	Q36L98_MARHY	Q36l98 marinobacte	382	61	13.2	200	2	Q3GEF5_9FIRM	Q3gef5 syntrophomo
310	61.5	13.3	134	2	Q6TSM0_9BACI	Q6tsm0 bacillus sp	383	61	13.2	238	2	Q5V6G2_HALMA	Q5v6g2 haloarcula
311	61.5	13.3	178	2	Q83E78_COXBU	Q83e78 coxiella bu	384	61	13.2	268	2	Q9AB59_CAUCR	Q9ab59 caulobacter
312	61.5	13.3	180	2	Q615L4_ORYZA	Q615l4 oryza sativ	385	61	13.2	272	2	Q8G9V3_ECOLI	Q8g9v3 escherichia
313	61.5	13.3	206	2	Q5JEL8_PYRKO	Q5jel8 pyrococcus	386	61	13.2	302	2	Q54880_RAT	Q54880 rattus norv
314	61.5	13.3	210	2	Q636E4_BACCC	Q636e4 bacillus ce	387	61	13.2	320	2	Q34086_COCER	Q34086 coccyzus er
315	61.5	13.3	213	2	Q8FR74_COREF	Q8fr74 corynebacte	388	61	13.2	326	2	Q3TXR0_MOUSE	Q3txr0 mus musculu
316	61.5	13.3	216	2	Q4NJJ0_9MLCC	Q4njj0 arthrobacte	389	61	13.2	326	2	Q762D5_MOUSE	Q762d5 m udp-glucu
317	61.5	13.3	216	2	Q7V8X4_PROMM	Q7v8x4 prochloroco	390	61	13.2	338	1	IGT_TREDE	P60974 treponema d
318	61.5	13.3	260	2	Q89N10_BRAJAZ	Q89n10 bradyrhizob	391	61	13.2	341	1	PAX5_SAGOE	Q2v156 sagittinus oe
319	61.5	13.3	262	2	Q9NB91_AGRIP	Q9nb91 agrotis ips	392	61	13.2	355	2	Q95592_COTJUA	Q95592 coturnix co
320	61.5	13.3	301	2	Q55KX5_CRYNE	Q55kx5 cryptococcu	393	61	13.2	380	2	Q7FG49_ANOGA	Q7fg49 anopheles g
321	61.5	13.3	301	2	Q5KAK4_CRYNE	Q5kak4 cryptococcu	394	61	13.2	389	2	Q7T197_CHICK	Q7t197 gallus gall
322	61.5	13.3	316	2	Q2WJL3_CLOBE	Q2wj3 clostridium	395	61	13.2	395	2	Q988F9_RHIL0	Q988f9 rhizobium l
323	61.5	13.3	330	2	Q6LFF1_PHOPR	Q6lff1 photobacter	396	61	13.2	413	2	Q59KD6_CANAL	Q59kd6 candida alb

105	66.5	14.4	523	1	KCNA3_HUMAN	P22001	homo sapien	178	63.5	13.8	141	2	Q3FWF6_9BURK	Q3fwf6 rhodofera
106	66.5	14.4	546	2	Q5RA50_PONPY	Q5ra50 pongo pygma	179	63.5	13.8	240	2	Q49XK1_PSEPU	Q49xf1 pseudomonas	
107	66.5	14.4	549	2	Q85W6_SHEON	Q8esw6 shewanella	180	63.5	13.8	241	2	Q5UX90_HALMA	Q5ux90 haloarcula	
108	66.5	14.4	557	2	Q6P2D3_HUMAN	Q6p2d3 homo sapien	181	63.5	13.8	244	2	Q39L16_BURSA	Q39l16 burkholderi	
109	66.5	14.4	575	2	Q5VMN2_HUMAN	Q5vmn2 homo sapien	182	63.5	13.8	284	2	Q41ZB5_DESHA	Q41zes desulfitoba	
110	66.5	14.4	767	2	Q2Y8H1_NITMU	Q2y8h1 nitrosospir	183	63.5	13.8	309	2	Q8Y5P7_LISMO	Q8y5p7 listeria mo	
111	66	14.3	139	2	Q5XWNO_SOLTU	Q5xwn0 solanum tub	184	63.5	13.8	309	2	Q92A05_LISIN	Q92a05 listeria in	
112	66	14.3	321	2	Q5S122_9BRAD	Q5s122 bradyrhizob	185	63.5	13.8	312	2	Q4EQD2_LISMO	Q4eqd2 listeria mo	
113	66	14.3	446	2	Q97UY7_SULSO	Q97uy7 sulfolobus	186	63.5	13.8	318	2	Q41G61_GIBZE	Q41g61 gibberella	
114	66	14.3	688	2	Q31168_PSEHT	Q31168 pseudoalter	187	63.5	13.8	327	2	Q6ZVM5_HUMAN	Q6zvm5 homo sapien	
115	65.5	14.2	161	2	Q5SN36_CRYNE	Q5sn36 cryptococcu	188	63.5	13.8	359	2	Q822F8_CHLCV	Q822f8 chlamydophi	
116	65.5	14.2	161	2	Q5KBG5_CRYNE	Q5kbg5 cryptococcu	189	63.5	13.8	372	2	Q5X4P4_LEGPA	Q5x4p4 legionella	
117	65.5	14.2	305	2	Q74DY6_GEOSL	Q74dy6 geobacter s	190	63.5	13.8	396	2	Q5UVL7_9PEZI	Q5uvl7 cercophora	
118	65.5	14.2	310	2	Q2JVO7_9CYAN	Q2jvq7 cyanobacter	191	63.5	13.8	410	2	Q4LUJ0_9BURK	Q4luj0 burkholderi	
119	65.5	14.2	333	2	Q6L3P2_SOLDI	Q6l3p2 solanum dem	192	63.5	13.8	420	2	Q6I568_ORYSA	Q6i568 oryza sativ	
120	65.5	14.2	374	2	Q2QR83_ORYSA	Q2qr83 oryza sativ	193	63.5	13.8	452	2	Q6FVH0_CANGA	Q6fvh0 candida gia	
121	65.5	14.2	428	2	Q4OKM9_DESAC	Q4okm9 desulfuromo	194	63.5	13.8	455	2	Q3F9X8_9BURK	Q3f9x8 burkholderi	
122	65.5	14.2	546	2	Q86V42_HUMAN	Q86v42 homo sapien	195	63.5	13.8	479	2	Q3TR92_MOUSE	Q3tr92 mus musculu	
123	65.5	14.2	546	2	Q96N39_HUMAN	Q96nj9 homo sapien	196	63.5	13.8	502	2	Q459G4_9BURK	Q459g4 burkholderi	
124	65.5	14.2	582	2	Q8N8P9_HUMAN	Q8n8p9 homo sapien	197	63.5	13.8	511	1	KCNC1_HUMAN	P48547 homo sapien	
125	65.5	14.2	1185	2	Q8SG58_SHEON	Q8sg58 shewanella	198	63.5	13.8	511	1	KCNC1_MOUSE	P15388 mus musculu	
126	65.5	14.2	1278	2	Q4SW90_TETNG	Q4sw90 tetraodon n	199	63.5	13.8	511	2	Q3KN38_HUMAN	Q3kns8 homo sapien	
127	65	14.1	100	2	Q2ITAI_RHOPA	Q2ital rhodopseudo	200	63.5	13.8	511	2	Q5BN35_RABIT	Q5bn35 oryctolagus	
128	65	14.1	134	2	Q5RI57_BRARE	Q5ri57 brachydanio	201	63.5	13.8	511	2	Q5BN36_BOVIN	Q5bn36 bos taurus	
129	65	14.1	327	2	Q9LVG3_ARATH	Q9lvq3 arabidopsis	202	63.5	13.8	511	2	Q3UHB6_MOUSE	Q3uhb6 m adult mal	
130	65	14.1	427	2	Q4U9T1_THEAN	Q4u9t1 theileria a	203	63.5	13.8	521	2	Q4V7K2_XENLA	Q4v7k2 xenopus lae	
131	65	14.1	469	2	Q9XDX1_MAGMG	Q9xdx1 magnetospir	204	63.5	13.8	550	2	Q4QEW8_9PARA	Q4qew8 measles vir	
132	65	14.1	582	2	Q5UQ22_MINIV	Q5uq22 minivir	205	63.5	13.8	564	2	Q2UHF4_ASPOR	Q2uhf4 aspergillus	
133	65	14.1	730	2	Q90638_CHICK	Q90638 gallus gall	206	63.5	13.8	585	1	KCNC1_RAT	P25122 rattus norv	
134	65	14.1	832	2	Q4BSB0_TETNG	Q4bsb0 tetraodon n	207	63.5	13.8	585	2	Q9XSJ8_CANFA	Q9xsj8 canis fami	
135	64.5	14.0	155	2	Q9R126_MOUSE	Q9r126 mus musculu	208	63.5	13.8	620	2	Q07239_MYCTU	Q07239 mycobacteri	
136	64.5	14.0	189	2	Q6C1N8_YARLI	Q6c1n8 yarrowia li	209	63.5	13.8	620	2	Q7U2A5_MYCBO	Q7u2a5 mycobacteri	
137	64.5	14.0	244	2	Q72EX5_DESVH	Q72ex5 desulfovibr	210	63.5	13.8	642	2	Q4SZN6_TETNG	Q4szn6 tetraodon n	
138	64.5	14.0	311	2	Q4HB57_LISMO	Q4hb57 deinococcus	211	63.5	13.8	644	2	Q35Q84_9BRAD	Q35q84 bradyrhizob	
139	64.5	14.0	312	2	Q4HEH0_LISMO	Q4heh0 listeria mo	212	63.5	13.8	725	2	Q4HL36_CAMLA	Q4hl36 campylobact	
140	64.5	14.0	372	2	Q71Y12_LISMF	Q71y12 listeria mo	213	63.5	13.8	747	2	Q57527_MAZE	Q57527 zea mays (m	
141	64.5	14.0	372	2	Q5WW34_LEGPL	Q5ww34 legionella	214	63.5	13.8	909	2	Q4DA40_TRYCR	Q4da40 trypanosoma	
142	64.5	14.0	416	2	Q3NLN2_SHEFR	Q3nl2 shewanella	215	63	13.7	80	2	Q7NU33_CHRVO	Q7nu33 chromobacte	
143	64.5	14.0	448	2	Q3NB05_PROAT	Q3nb05 nitrosomona	216	63	13.7	125	2	Q5UJ33_PYRKO	Q5uj33 pyrococcus	
144	64.5	14.0	452	2	Q7T165_BRARE	Q7t165 brachydanio	217	63	13.7	194	2	Q3BX62_XANC5	Q3bx62 xanthomonas	
145	64.5	14.0	455	2	Q8TZX5_PYRPU	Q8tzx5 pyrococcus	218	63	13.7	201	2	Q31NJ4_SYNP7	Q31nj4 synechococc	
146	64.5	14.0	465	2	Q86080_RHOSH	Q86080 rhodobacter	219	63	13.7	201	2	Q5N5M0_SYNP6	Q5nm50 synechococc	
147	64.5	14.0	465	2	Q3IXA5_RHOSA	Q3ixa5 rhodobacter	220	63	13.7	339	2	Q3GZT7_9ACTO	Q3gzt7 nocardioid	
148	64.5	14.0	550	2	Q9QEW7_9PARA	Q9qew7 measles vir	221	63	13.7	378	2	Q7QFG1_ANOGA	Q7qfg1 anopheles g	
149	64.5	14.0	550	2	Q9QEW9_9PARA	Q9qew9 measles vir	222	63	13.7	417	2	Q375X8_RHOPA	Q375x8 rhodopseudo	
150	64.5	14.0	633	2	Q4SHG0_TETNG	Q4shg0 tetraodon n	223	63	13.7	465	2	Q4PDK1_USTMA	Q4pdk1 ustilago ma	
151	64.5	14.0	677	2	Q5GUQ5_XANOR	Q5guq5 xanthomonas	224	63	13.7	467	2	Q4I5E1_GIBZE	Q4i5e1 gibberella	
152	64.5	14.0	725	2	Q8SY05_DROME	Q8sy05 drosophila	225	63	13.7	468	2	Q9ZVA7_ARATH	Q9zva7 arabidopsis	
153	64.5	14.0	871	2	Q5A4X3_CANAL	Q5a4x3 candida alb	226	63	13.7	496	2	Q7NB28_MYCGA	Q7nb28 mycoplasma	
154	64.5	14.0	920	2	Q6XR97_9BACT	Q6xr97 uncultured	227	63	13.7	622	2	Q59QV3_CANAL	Q59qv3 candida alb	
155	64.5	14.0	1750	2	Q4WRV3_ASPFU	Q4wrv3 aspergillus	228	63	13.7	655	2	Q8KW19_STRMU	Q8kw19 streptococc	
156	64.5	14.0	2281	2	Q3F3Z0_9BURK	Q3f3z0 burkholderi	229	63	13.7	655	2	Q8DUN3_CANAL	Q8dun3 streptococc	
157	64	13.9	186	2	Q4RHT5_TETNG	Q4rht5 tetraodon n	230	63	13.7	750	2	Q59R09_CANAL	Q59r09 candida alb	
158	64	13.9	244	2	Q4BB11_BURVI	Q4bb11 burkholderi	231	63	13.7	808	2	Q6DD69_XENLA	Q6dd69 xenopus lae	
159	64	13.9	250	2	Q7WU64_9THEM	Q7wu64 thermotoga	232	63	13.7	825	2	Q933G5_9GAMA	Q933g5 callitrichi	
160	64	13.9	303	2	Q4KGC4_PSEF5	Q4kgc4 pseudomonas	233	63	13.7	912	2	Q8D4M3_VIBVU	Q8d4m3 vibrio vuln	
161	64	13.9	315	2	Q9LS88_ARATH	Q9ls88 arabidopsis	234	63	13.7	917	2	Q5E8X2_VIBF1	Q5e8x2 vibrio fisc	
162	64	13.9	340	2	Q72W35_LEPIC	Q72w35 leptospira	235	63	13.7	923	2	Q9N389_CABEL	Q9n389 caenorhabdi	
163	64	13.9	383	2	Q6N5J0_RHOPA	Q6n5j0 rhodopseudo	236	63	13.7	1022	2	Q27779_SCHMA	Q27779 schistosoma	
164	64	13.9	436	2	Q86VR7_HUMAN	Q86vr7 homo sapien	237	63	13.7	1411	2	Q5AS38_EMENI	Q5as38 aspergillus	
165	64	13.9	524	2	Q475P1_RALEJ	Q475p1 ralstonia e	238	62.5	13.6	146	2	Q81GV1_BACCR	Q81gv1 bacillus ce	
166	64	13.9	525	1	KCNA3_RAT	P15384 rattus norv	239	62.5	13.6	148	2	Q3E2R6_BACTI	Q3e2r6 bacillus th	
167	64	13.9	582	2	Q6K620_ORYSA	Q6k620 oryza sativ	240	62.5	13.6	160	2	Q3E2R6_BACTI	Q3e2r6 schistosoma	
168	64	13.9	667	2	Q9BJM1_TRISP	Q9bjm1 trichinella	241	62.5	13.6	163	2	Q73CB6_BACCA	Q73cb6 bacillus ce	
169	64	13.9	678	2	Q8R9G1_THETN	Q8r9g1 thermoanaer	242	62.5	13.6	174	2	Q3Q4C2_9GAMM	Q3q4c2 shewanella	
170	64	13.9	727	2	Q6FIK3_CANGA	Q6fik3 candida gla	243	62.5	13.6	207	2	Q8TBL6_HUMAN	Q8tbl6 homo sapien	
171	64	13.9	774	2	Q3JTQ0_BURP1	Q3jtq0 burkholderi	244	62.5	13.6	286	2	Q9SB33_HUMAN	Q9sb33 homo sapien	
172	64	13.9	804	2	Q7SGV0_ORYSA	Q7sgv0 oryza sativ	245	62.5	13.6	299	1	COMQ_BACSU	P33690 bacillus su	
173	64	13.9	915	2	Q7MG71_VIBVY	Q7mg71 vibrio vuln	246	62.5	13.6	339	1	TMW66_HUMAN	Q96by9 homo sapien	
174	64	13.9	1046	2	Q82WK5_NITEU	Q82wk5 nitrosomona	247	62.5	13.6	372	2	Q5ZUY1_LEGPH	Q5zuy1 legionella	
175	64	13.9	1155	2	Q2NT22_SODGL	Q2nt22 sodalis glo	248	62.5	13.6	434	2	Q6HHZ7_BACPK	Q6hhz7 bacillus th	
176	63.5	13.8	63	2	Q3CK79_THETN	Q3ck79 thermoanaer	249	62.5	13.6	434	2	Q81PR7_BACAN	Q81pr7 bacillus an	
177	63.5	13.8	83	2	Q41HR9_9BACI	Q41hr9 exiguobacte	250	62.5	13.6	492	2	Q750E3_ASHGO	Q750e3 ashbya goss	

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OM protein - protein search, using sw model

Run on: November 21, 2006, 19:46:39 ; Search time 301 Seconds
(without alignments)
273.510 Million cell updates/sec

Title: US-10-063-557-50
Perfect score: 461
Sequence: 1 MERVYIALLLAGLTALLEAN.....HSPVPEKAIPITPGSATTC 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Uniprot 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461	100.0	89	Q6UWZ1	HUMAN
2	452	98.0	89	Q7Z4M5	HUMAN
3	450	97.6	89	FXYP4	HUMAN
4	276.5	60.0	88	FXYP4	MOUSE
5	256.5	55.6	87	FXYP4	RAT
6	241.5	52.4	88	FXYP3	MOUSE
7	241.5	52.4	88	FXYP3	MOUSE
8	234.5	50.9	88	FXYP3	RAT
9	230.5	50.0	88	FXYP3	HUMAN
10	214.5	46.5	87	FXYP3	HUMAN
11	214.5	46.5	87	Q6IB59	MOUSE
12	203	44.0	70	Q80UV3	BOVIN
13	131.5	28.5	92	Q3SZX0	BOVIN
14	129	28.0	92	PLM	HUMAN
15	127.5	27.7	88	Q4RFG2	TETNG
16	126.5	27.4	92	PLM	CANFA
17	124.5	27.0	94	FXYP6	RAT
18	123.5	26.8	94	FXYP6	MOUSE
19	119	25.8	100	Q5MBE9	XENTLA
20	116.5	25.3	95	Q3MZ55	BOVIN
21	116	25.2	94	Q70Q12	SQUAC
22	115.5	25.1	92	PLM	MOUSE
23	115	24.9	95	FXYP6	PONPY
24	113.5	24.6	95	Q6DJF4	XENTLA
25	113	24.5	92	PLM	RAT
26	112.5	24.4	95	FXYP6	HUMAN
27	112.5	24.4	95	FXYP6	MACACA
28	110	23.9	95	Q5ZM59	CHICK
29	107.5	23.3	87	Q4RHT7	TETNG
30	103.5	22.5	94	Q6JDJ6	XENTLA
31	96.5	20.9	58	ATNG	BOVIN

32	96	20.8	99	2	Q7SZ52	BRARE
33	95.5	20.7	53	1	ATNG	SHEEP
34	95.5	20.7	65	2	Q58K79	PIG
35	94	20.4	178	1	FXYP5	HUMAN
36	93	20.2	178	2	Q3TDM1	MOUSE
37	92	20.0	178	1	FXYP5	RAT
38	92	20.0	178	2	Q6P9W0	RAT
39	89.5	19.4	78	2	Q3ZBJ3	BOVIN
40	89	19.3	80	1	FXYP7	HUMAN
41	85	18.4	80	1	FXYP7	MOUSE
42	84	18.2	178	2	Q8IWS1	HUMAN
43	83	18.0	66	1	ATNG	HUMAN
44	83	18.0	80	1	FXYP7	RAT
45	83	18.0	94	1	FXYP8	HUMAN
46	82.5	17.9	66	1	ATNG	RAT
47	79.5	17.2	142	2	Q6P8R9	MOUSE
48	78	16.9	70	1	ATNG	MOUSE
49	78	16.9	70	2	Q6ITT2	MOUSE
50	77.5	16.8	711	2	Q4NGJ7	9MIC
51	76	16.5	289	2	Q4WU10	ASPFU
52	75.5	16.4	524	2	Q5LOV1	SILPO
53	74	16.1	188	2	Q5LW65	SILPO
54	74	16.1	208	2	Q4R6E0	MACFA
55	73.5	15.9	64	2	Q6ITT1	MOUSE
56	73.5	15.9	82	2	Q6ITT0	MOUSE
57	73.5	15.9	196	2	Q9CZB7	CABEL
58	73.5	15.9	330	2	Q84EY9	ENTCL
59	73	15.8	201	2	Q7QJ63	ANOGA
60	73	15.8	455	2	Q4IPU0	GIBZE
61	73	15.8	1132	2	Q83861	9REOV
62	72	15.6	160	1	PTD	SYNY3
63	71	15.4	61	1	ATNG	XENLA
64	71	15.4	529	2	Q34355	BACSU
65	71	15.4	577	2	Q4A723	MYCS5
66	70.5	15.3	251	2	Q54FJ8	DICD1
67	70.5	15.3	334	2	Q6D644	ERWCT
68	70	15.2	184	1	FXYP5	MOUSE
69	70	15.2	216	2	Q5ZFS6	PLAMJ
70	69.5	15.1	236	2	Q6GME4	XENLA
71	69.5	15.1	268	2	Q4PSL8	PSYAR
72	69.5	15.1	458	2	Q5KUP7	GEOKA
73	69	15.0	150	2	Q668G1	YERPS
74	69	15.0	150	2	Q8ZCD4	YERPE
75	69	15.0	157	2	Q8D0Y1	YERPE
76	68.5	14.9	146	2	Q36ZKX	RIOPA
77	68.5	14.9	339	2	Q94E19	ARATH
78	68.5	14.9	340	2	Q3X714	METFL
79	68.5	14.9	346	2	Q9CL30	PASMU
80	68.5	14.9	456	2	Q58EK5	BRARE
81	68.5	14.9	499	2	Q5VHU5	CIOIN
82	68.5	14.9	531	2	Q5VHU5	CIOIN
83	68.5	14.9	531	2	Q8HKR3	9PERC
84	68	14.8	417	2	Q4QD23	LEIMA
85	68	14.8	978	2	Q69SP5	ORYSA
86	68	14.8	135	1	YCF66	MARPO
87	67.5	14.6	216	2	Q3EKS3	BACTI
88	67.5	14.6	227	2	Q37UP8	SPHAR
89	67.5	14.6	337	2	Q6L3V4	SOLDE
90	67.5	14.6	387	2	Q6YYV7	ORYSA
91	67.5	14.6	664	1	RN139	HUMAN
92	67.5	14.6	664	2	Q5RBT7	PONPY
93	67.5	14.6	664	2	Q2W8Y8	MAGSA
94	67	14.5	227	2	Q2W8Y8	MAGSA
95	67	14.5	364	2	Q5ZFS7	PLAMJ
96	67	14.5	390	1	AROC	SULTO
97	67	14.5	715	2	Q72E54	DESVH
98	66.5	14.4	174	2	Q3PM00	NITHA
99	66.5	14.4	241	2	Q9K113	STRCO
100	66.5	14.4	263	2	Q4B4Z0	9BURK
101	66.5	14.4	329	2	Q6OD39	SOLTU
102	66.5	14.4	359	1	AROC	CHLNP
103	66.5	14.4	408	2	Q3PM48	NITHA
104	66.5	14.4	516	2	Q28656	RABIT

Q7az52	brachydanio
Q04680	ovis aries
Q58K79	sus scrofa
Q96db9	homo sapien
Q3cdw1	m nod-deriv
P59647	rattus norv
Q6P9W0	rattus norv
Q3ZBJ3	bos taurus
P59549	homo sapien
P59648	mus musculus
Q8IWS1	homo sapien
P54710	homo sapien
P59649	rattus norv
P59550	homo sapien
Q04679	rattus norv
Q6P8R9	mus musculus
Q04646	mus musculus
Q6ITT2	mus musculus
Q4NGJ7	arthrobacte
Q4WU10	aspergillus
Q5LQV1	silicibacte
Q5LW65	silicibacte
Q4R6E0	macaca fasc
Q6ITT1	mus musculus
Q6ITT0	mus musculus
Q9CZB7	caenorhabdi
Q84EY9	enterobacte
Q7QJ63	anopheles g
Q4IPU0	gibberella
Q83861	niilaparvata
P27589	synecocyst
Q13001	xenopus lae
Q34355	bacillus su
Q4A723	mycoplasma
Q54FJ8	dictyosteli
Q6D644	erwinia car
P97808	mus musculus
Q5ZFS6	plantaio ma
Q6GME4	xenopus lae
Q4F818	psychrobact
Q5KUP7	geobacillus
Q668G1	yersinia ps
Q8ZCD4	yersinia pe
Q8D0Y1	yersinia pe
Q36ZKX	rhodopseudo
Q94E19	arabidopsis
Q3X714	methylobacti
Q9CL30	pasteurella
Q58EK5	brachydanio
Q5VHU4	ciona intes
Q5VHU5	ciona intes
Q8HKR3	arcos sp. k
Q4QD23	leishmania
Q69SP5	oryza sativ
YCF66	marchantia
Q32616	marchantia
Q3EKS9	bacillus th
Q37UP8	novospingo
Q6L3V4	solanum dem
Q6YYV7	oryza sativ
Q8WU17	homo sapien
Q5RBT7	pongo pygma
Q2W8Y8	magnetospir
Q5ZFS7	plantaio ma
Q96Y94	sulfolobus
Q72E54	desulfovibr
Q3PM00	nitrobacter
Q9K113	streptomyce
Q4B4Z0	polaromonas
Q6OD39	solanum tub
Q9Z639	chlamydia p
Q3PM48	nitrobacter
Q28656	oryctolagus

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J. Biol. Chem. 267, 8650-8657, 1992
A;Title: Cloning, functional expression, and regulation of two K(+) channels in human T
A;Reference number: A38101; MUID:92235098; PMID:1373731
A;Accession: A38101
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-523 <ATT>
A;Cross-references: UNIPROT:P22001; UNIPARC:UPI000016AB94; GB:M85217; NID:g186664; PIDN:
R;Phillipson, L.H.; Hice, R.E.; Schaefer, K.; LaMendola, J.; Bell, G.I.; Nelson, D.J.; Sc
Proc. Natl. Acad. Sci. U.S.A. 88, 53-57, 1991
A;Title: Sequence and functional expression in Xenopus oocytes of a human insulinoma and
A;Reference number: A38556; MUID:91095456; PMID:1986382
A;Accession: B38556
A;Molecule type: DNA
A;Residues: 1-19, G', 21-36, 'V', 38-60, 'L', 62-90, 'V', 92-337, 'S', 339-418, 'S', 420-457, 'LS', 4
A;Cross-references: UNIPARC:UPI00001779F2; GB:M55515
R;Cai, Y.C.; Osborne, P.B.; North, R.A.; Dooley, D.C.; Douglass, J.
DNA Cell Biol. 11, 163-172, 1992
A;Title: Characterization and functional expression of genomic DNA encoding the human ly
A;Reference number: I52990; MUID:92189730; PMID:1547020
A;Accession: I52990
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-60, 'L', 62-523 <RES>
A;Cross-references: UNIPARC:UPI0000001C29; GB:M38217; NID:g186670; PIDN:AAB88073.1; PID:
C;Genetics:
A;Gene: GDB:KCNJ3; HGK5
A;Cross-references: GDB:128079; OMIM:176263
A;Map position: lp21-lp13.3
C;Superfamily: potassium channel protein drk1
C;Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; volt

Query Match 14.4% Score 66.5; DB 2; Length 523;
Best Local Similarity 20.1%; Pred. No. 19;
Matches 30; Conservative 14; Mismatches 36; Indels 69; Gaps 5;
Qy 8 LLLLAGLTALNDP---FANKDDP-----YYDWKNLQLSLGICGGLAAGI 53
Db 358 ILFSSAVYFAEADDPSTGFSIPDAFWAVVMTVTGVDGMDHPVTIGGKIVGSLCAIAGV 417
Qy 54 AAVL-----SGKCKYKSSQKQ----- 69
Db 418 LTIALPVPVIVSNFYHRETEGEESQYMHVGSCHLSSAEELRKARNSNLSKSEY 477
Qy 70 -----HSPVPEKAIPILTPGSATTC 89
Db 478 MWIEGGGMHSAFPQ--TFEKTGNSTATC 504

Search completed: November 21, 2006, 19:47:27
Job time : 76 secs

[illegible]

Db 1 MQEVLVLLVLAGLPTLDNDP-ENKNDPFYDYWYSLRVGGLICAGLICALGIIVLMSG 59

QY 60 KKKYSSQKHSPVPEKAIPLTPGSATTC 89
||| ||| ||| : ||||| |
Db 60 KCKCKFRQKP-SHRPGEGPLTPGSAHNC 88
||| ||| ||| : ||||| |

RESULT 3
A55571
Chloride conductance inducer Mat-8 - human
C:Species: Homo sapiens (man)
C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A55571
R:Morrisson, B.W.; Moorman, J.R.; Kowdley, G.C.; Kobayashi, Y.M.; Jones, L.R.; Leder, P.
J. Biol. Chem. 270, 2176-2182, 1995
A:Title: Mat-8, a novel phospholipase-like protein expressed in human breast tumors, and
A:Reference number: A55571; MUID:95138184; PMID:7836447
A:Accession: A55571
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-87 <MOR>
A:Cross-references: UNIPROT:Q14802; UNIPARC:UPI0000052765; GB:S74645; NID:g10
C:Keywords: transmembrane protein

Query Match 46.5%; Score 214.5; DB 2; Length 87;
Best Local Similarity 54.5%; Pred. No. 1.2e-16;
Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;

QY 1 MERVTLALL-LAGLTALRANDPFANKDDPFYDWKNLQSLGGLAIAAGIAVLGSG 59
||| ||| ||| : ||||| |
Db 1 MQKVTGLLVLAGLPVFDAND-LEDKNSPFYDWHSLQVGLGICAGVLCANGIIVMSA 59
||| ||| ||| : ||||| |

QY 60 KKKYSSQKQ-HSPVPEKAIPLTPGSA 86
||| ||| ||| : ||||| |
Db 60 KCKCKFGQKSGHH--PGETPPLITPGSA 85
||| ||| ||| : ||||| |

RESULT 4
A40533
cAMP-dependent protein kinase major membrane substrate precursor - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 09-Jul-2004
C:Accession: A40533
R:Palmer, C.J.; Scott, B.T.; Jones, L.R.
J. Biol. Chem. 266, 11126-11130, 1991
A:Title: Purification and complete sequence determination of the major plasma membrane
A:Reference number: A40533; MUID:91250422; PMID:1710217
A:Accession: A40533
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <PAL>
A:Cross-references: UNIPROT:P56513; UNIPARC:UPI0000131C15; GB:M63934

Query Match 27.4%; Score 126.5; DB 2; Length 92;
Best Local Similarity 41.4%; Pred. No. 7.1e-07;
Matches 29; Conservative 15; Mismatches 23; Indels 3; Gaps 2;

QY 8 LLLLAG-LTALRANDPFANKDDPFYDWKNLQSLGGLAIAAGIAVLGSKCKYKSS 66
||| ||| ||| : ||||| |
Db 8 LVLCVGLTATAEAP--QEHDPFTYDQSLRIGGLIAGILFILGILVLSRRCKFN 65
||| ||| ||| : ||||| |

QY 67 QKHSPVPEK 76
||| ||| ||| : ||||| |
Db 66 QOQRTGEPE 75
||| ||| ||| : ||||| |

RESULT 5
D46435
Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: D46435; S31525
R:Mercer, R.W.; Biemesderfer, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.

J. Cell Biol. 121, 579-586, 1993
A:Title: Molecular cloning and immunological characterization of the gamma polypeptide, a
A:Reference number: A46435; MUID:93252993; PMID:8387529
A:Accession: D46435
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-58 <MER>
A:Cross-references: UNIPROT:Q04645; UNIPARC:UPI00001262A7; EMBL:X70059; NID:g396; PIDN:CJ
A>Note: the authors translated the codon TTC for residue 25 as Pro
C:Keywords: hydrolase; transmembrane protein

Query Match 20.9%; Score 96.5; DB 2; Length 58;
Best Local Similarity 34.6%; Pred. No. 0.00092;
Matches 18; Conservative 14; Mismatches 19; Indels 1; Gaps 1;

QY 27 DDPFYDWKNLQSLGGLAIAAGIAVLGSKCKYKSSQKHSPVPEKAI 78
||| ||| ||| : ||||| |
Db 8 EDPFYDYETVRNGGLIIPAALAFIVGLVLIILSKRFRG-GAKKQHRQIPEDGL 58
||| ||| ||| : ||||| |

RESULT 6
A46435
Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - sheep (fragment)
N:Alternate names: sodium pump gamma chain; sodium/potassium-dependent
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 22-Nov-1993 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
R:Mercer, R.W.; Biemesderfer, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.
J. Cell Biol. 121, 579-586, 1993
A:Title: Molecular cloning and immunological characterization of the gamma polypeptide, a
A:Reference number: A46435; MUID:93252993; PMID:8387529
A:Accession: A46435
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 6-53 <MER>
A:Cross-references: UNIPROT:Q04680; UNIPARC:UPI000017CC97
A:Experimental source: kidney
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBI:131232, NCBI:131233)
R:Mercer, R.W.
submitted to the EMBL Data Library, December 1992
A:Description: Cloning and sequencing of gamma subunit of sodium potassium ATPase.
A:Reference number: S31522
A:Accession: S31524
A:Molecule type: mRNA
A:Residues: 6-19, 'F', 21-53 <NEW>
A:Cross-references: UNIPARC:UPI000016C4B7; EMBL:X70061; NID:g1255; PIDN:CAA49665.1; PID:9
R:Collins, J.H.; Leszyk, J.
Biochemistry 26, 8665-8668, 1987
A:Title: The "gamma-subunit" of Na,K-ATPase: a small, amphiphilic protein with a unique
A:Reference number: A27383; MUID:88163944; PMID:2831947
A:Accession: A27383
A:Molecule type: protein
A:Residues: 1-19, 'F', 21-33 <COL>
A:Cross-references: UNIPARC:UPI000017CC98
C:Complex: heterotrimer; alpha, beta, and gamma chain
C:Keywords: heterotrimer; hydrolase; transmembrane protein

Query Match 20.5%; Score 94.5; DB 2; Length 53;
Best Local Similarity 34.6%; Pred. No. 0.0014;
Matches 18; Conservative 14; Mismatches 19; Indels 1; Gaps 1;

QY 27 DDPFYDWKNLQSLGGLAIAAGIAVLGSKCKYKSSQKHSPVPEKAI 78
||| ||| ||| : ||||| |
Db 3 EDPFYDYETVRNGGLIIPAALAFIVGLVLIILSKRFRG-GAKKQHRQIPEDGL 53
||| ||| ||| : ||||| |

RESULT 7
B46435
Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: B46435; S31523

1271	49	10.6	618	2	F84409	arsenite transport	1344	48.5	10.5	269	2	G87134	enoyl-[ACP] reduct
1272	49	10.6	629	2	S29685	retroviral recepto	1345	48.5	10.5	273	2	JS0172	chlorophyll a/b-bi
1273	49	10.6	640	2	S29685	threonine-trna lig	1346	48.5	10.5	276	2	D41044	octopine-binding p
1274	49	10.6	660	2	C84944	xanthophyll epoxid	1347	48.5	10.5	277	2	D64666	glutamine ABC tran
1275	49	10.6	672	2	A65024	hydrogenase-4 comp	1348	48.5	10.5	278	2	G71849	amino acid ABC tra
1276	49	10.6	672	2	D85891	hydrogenase-4 memb	1349	48.5	10.5	278	2	AB2254	hypothetical prote
1277	49	10.6	672	2	H91046	hydrogenase-4 memb	1350	48.5	10.5	283	2	B86331	F6f9.15 protein -
1278	49	10.6	680	2	T29871	hypothetical prote	1351	48.5	10.5	283	2	D71130	probable oligopept
1279	49	10.6	719	2	S63392	probable membrane	1352	48.5	10.5	290	2	F71167	hypothetical prote
1280	49	10.6	740	2	T03847	Fas-binding protei	1353	48.5	10.5	291	2	F81444	probable integral
1281	49	10.6	748	1	I50699	cytosolic phosphol	1354	48.5	10.5	302	2	A75432	3-hydroxybutyryl-C
1282	49	10.6	784	2	JH0101	apolipoprotein B-1	1355	48.5	10.5	312	2	I40201	mgE protein - Bac
1283	49	10.6	796	2	E87636	TonB-dependent rec	1356	48.5	10.5	318	2	B91177	probable hemin per
1284	49	10.6	799	2	T48690	hypothetical prote	1357	48.5	10.5	330	2	C86023	hypothetical prote
1285	49	10.6	812	2	AG3138	fimbrial usher pro	1358	48.5	10.5	332	2	AC0260	hypothetical phage
1286	49	10.6	812	2	D98149	hypothetical prote	1359	48.5	10.5	334	2	C81794	hypothetical prote
1287	49	10.6	816	2	T21713	hypothetical prote	1360	48.5	10.5	340	2	E83126	ferric enterobacti
1288	49	10.6	839	2	S35319	nucleoporin-intera	1361	48.5	10.5	342	2	E71359	hypothetical prote
1289	49	10.6	862	2	S64821	probable membrane	1362	48.5	10.5	355	2	T47527	hypothetical prote
1290	49	10.6	952	2	E84534	hypothetical prote	1363	48.5	10.5	365	2	F87552	dprA protein limpo
1291	49	10.6	969	2	F71418	hypothetical prote	1364	48.5	10.5	370	2	AE0289	conserved hypotet
1292	49	10.6	975	2	T22788	hypothetical prote	1365	48.5	10.5	372	2	C39371	Ig V-region-like B
1293	49	10.6	976	2	S40697	processing endopro	1366	48.5	10.5	382	2	A10040	probable methanol
1294	49	10.6	1041	2	B81281	probable secret	1367	48.5	10.5	387	2	H88012	protein K10B4.2 (i
1295	49	10.6	1054	2	T30933	chitinase (EC 3.2.	1368	48.5	10.5	388	2	T33908	hypothetical prote
1296	49	10.6	1073	1	OYHUHX	heat-stable entero	1369	48.5	10.5	394	2	AE1940	two-component resp
1297	49	10.6	1086	2	T40354	hypothetical prote	1370	48.5	10.5	398	2	F75417	L-sorbose dehydr
1298	49	10.6	1190	2	T00842	probable histidine	1371	48.5	10.5	400	2	AG1208	cell-division prot
1299	49	10.6	1207	2	T52459	sensory transducti	1372	48.5	10.5	400	2	AB1565	cell-division prot
1300	49	10.6	1230	2	S47466	cellulose 1,4-beta	1373	48.5	10.5	401	2	B72329	hypothetical prote
1301	49	10.6	1265	2	T51314	probable CO-induce	1374	48.5	10.5	406	2	T31778	hypothetical prote
1302	49	10.6	1296	2	S36851	L-shaped tail fibe	1375	48.5	10.5	409	2	B85735	probable membrane
1303	49	10.6	1430	2	AF0351	probable autotrans	1376	48.5	10.5	410	2	C86835	hypothetical prote
1304	49	10.6	1530	2	E82085	glutamate synthase	1377	48.5	10.5	416	2	T02194	probable pectinase
1305	49	10.6	1648	2	F84833	probable SNF2/SWI2	1378	48.5	10.5	421	2	E90883	hypothetical prote
1306	49	10.6	2172	2	T20145	hypothetical prote	1379	48.5	10.5	424	2	T31978	hypothetical prote
1307	49	10.6	3164	1	WMBBH6	UL36 protein - hum	1380	48.5	10.5	425	2	T25873	hypothetical prote
1308	48.5	10.5	73	2	D91146	hypothetical prote	1381	48.5	10.5	426	2	B75434	UDP-N-acetylglucos
1309	48.5	10.5	73	2	H85991	hypothetical prote	1382	48.5	10.5	426	2	F45767	hypothetical prote
1310	48.5	10.5	73	2	E65119	hypothetical 7.5 k	1383	48.5	10.5	428	2	J01864	hypothetical prote
1311	48.5	10.5	75	2	T45361	hypothetical prote	1384	48.5	10.5	431	2	H70731	probable esterase
1312	48.5	10.5	115	1	SPRGG	substance P gamma	1385	48.5	10.5	436	2	I39973	alkaline serine pr
1313	48.5	10.5	116	2	AD2124	hypothetical prote	1386	48.5	10.5	441	2	H98009	hypothetical prote
1314	48.5	10.5	139	2	G71033	hypothetical prote	1387	48.5	10.5	443	2	H70430	K+ transport prote
1315	48.5	10.5	146	1	A47481	interleukin-13 pre	1388	48.5	10.5	461	2	C98120	glycerol-3-phospha
1316	48.5	10.5	165	2	A31635	neural cell adhesi	1389	48.5	10.5	463	2	E81141	xanthine/uracil pe
1317	48.5	10.5	171	2	JE0153	mitochondrial inne	1390	48.5	10.5	467	2	T32292	hypothetical prote
1318	48.5	10.5	180	2	I40562	hypothetical 20.1K	1391	48.5	10.5	470	1	P2WL39	L2 protein - human
1319	48.5	10.5	183	2	B81237	hypothetical prote	1392	48.5	10.5	473	2	T17260	hypothetical prote
1320	48.5	10.5	183	2	G82008	probable integral	1393	48.5	10.5	475	2	T08753	hypothetical prote
1321	48.5	10.5	193	2	C97891	hypothetical prote	1394	48.5	10.5	478	2	D84895	probable membrane
1322	48.5	10.5	198	2	S75989	endopeptidase Clp	1395	48.5	10.5	500	2	AD1047	probable amino aci
1323	48.5	10.5	199	2	T38524	ATP synthase subun	1396	48.5	10.5	509	2	A96563	probable protein k
1324	48.5	10.5	199	2	A69859	hypothetical prote	1397	48.5	10.5	510	2	B72007	conserved hypotet
1325	48.5	10.5	208	2	C96997	protein K02B9.4 (i	1398	48.5	10.5	511	2	H90439	hypothetical prote
1326	48.5	10.5	211	2	C59091	hypothetical prote	1399	48.5	10.5	518	2	T05196	hypothetical prote
1327	48.5	10.5	217	2	A98196	hypothetical prote	1400	48.5	10.5	528	2	E81186	L-lactate permease
1328	48.5	10.5	221	2	D64907	membrane protein y	1401	48.5	10.5	537	2	A75123	proline permease (
1329	48.5	10.5	225	2	F81977	hypothetical prote	1402	48.5	10.5	546	1	VGNZRK	cell fusion glycop
1330	48.5	10.5	225	2	E86043	probable transposa	1403	48.5	10.5	546	2	S47305	gene F protein - r
1331	48.5	10.5	226	2	T23233	hypothetical prote	1404	48.5	10.5	553	2	C84920	hypothetical prote
1332	48.5	10.5	235	2	AC2809	conserved hypotet	1405	48.5	10.5	553	2	T06499	hypothetical prote
1333	48.5	10.5	235	2	H97587	hypothetical 25.1K	1406	48.5	10.5	556	2	S68408	hypothetical prote
1334	48.5	10.5	241	2	D84138	hypothetical prote	1407	48.5	10.5	559	2	C75286	methyl-accepting c
1335	48.5	10.5	243	2	B96010	conserved hypotet	1408	48.5	10.5	578	2	B82204	hypothetical prote
1336	48.5	10.5	245	2	E97425	flagellar biosynth	1409	48.5	10.5	583	2	A70723	probable acyl-coas
1337	48.5	10.5	245	2	AE2643	flagellar biosynth	1410	48.5	10.5	584	1	VCWSIA	env polyprotein pr
1338	48.5	10.5	256	2	D86544	NADH (ubiquinone)	1411	48.5	10.5	590	2	C86465	probable inositol
1339	48.5	10.5	256	2	H72078	probable sodium-tr	1412	48.5	10.5	598	2	A69609	carbon starvation
1340	48.5	10.5	257	2	A12741	conserved hypotet	1413	48.5	10.5	601	2	G96558	probable protein k
1341	48.5	10.5	257	2	H97522	hypothetical prote	1414	48.5	10.5	605	2	T15291	sphingomyelin phos
1342	48.5	10.5	257	2	G87509	hypothetical prote	1415	48.5	10.5	608	2	C95255	hypothetical prote
1343	48.5	10.5	258	2	H70487	cytochrome-c oxida	1416	48.5	10.5	610	2	A11110	two-component sens

1125	49.5	10.7	1461	2	A85547	hypothetical prote	1198	49	10.6	355	2	S41686	geranylgeranyltran
1126	49.5	10.7	1492	2	A39322	cystic fibrosis tr	1199	49	10.6	366	2	A64950	membrane-bound pen
1127	49.5	10.7	2150	2	T08165	RNA1 polypeptoin -	1200	49	10.6	366	2	C95800	probable cytochrom
1128	49.5	10.7	2222	1	A36028	DNA-directed DNA p	1201	49	10.6	366	2	G30951	probable cytochrom
1129	49.5	10.7	2403	2	T30875	PRP8 protein homol	1202	49	10.6	370	2	G96770	hypothetical prote
1130	49.5	10.7	2500	1	WMHUE2	HIV-EP2 enhancer-b	1203	49	10.6	370	2	AB0602	probable membrane
1131	49.5	10.7	3655	2	T38084	TRAP-like protein	1204	49	10.6	378	2	F64446	chorismate synthas
1132	49	10.6	98	2	T17363	NADH2 dehydrogenas	1205	49	10.6	379	2	E69332	heterodisulfide re
1133	49	10.6	98	2	T17177	NADH2 dehydrogenas	1206	49	10.6	380	2	T11033	ubiquinol-cytochro
1134	49	10.6	99	2	D75182	lsu ribosomal prot	1207	49	10.6	382	2	A82056	hypothetical prote
1135	49	10.6	129	2	T28983	hypothetical prote	1208	49	10.6	385	2	AB6227	hypothetical prote
1136	49	10.6	135	2	F86053	hypothetical prote	1209	49	10.6	391	2	T39673	probable mannosylt
1137	49	10.6	135	2	D91207	hypothetical prote	1210	49	10.6	396	2	T35024	probable glutathio
1138	49	10.6	135	2	A65171	ci35 protein - Esc	1211	49	10.6	400	2	C83511	flagellar protein
1139	49	10.6	137	1	JC4877	phospholipase A2 h	1212	49	10.6	404	2	B86962	probable secreted
1140	49	10.6	140	2	S74898	hypothetical prote	1213	49	10.6	408	2	A37813	UDP-N-acetylglucos
1141	49	10.6	146	2	T06471	core protein - gar	1214	49	10.6	411	2	S75327	lysothaphin - Syne
1142	49	10.6	154	2	C71379	probable ATPase, c	1215	49	10.6	419	1	S47692	hypothetical 43.8K
1143	49	10.6	157	2	S18651	variant surface an	1216	49	10.6	419	2	B91169	probable transport
1144	49	10.6	157	2	S58025	probable olfactory	1217	49	10.6	419	2	B86015	probable transport
1145	49	10.6	159	2	S77852	probable phenylala	1218	49	10.6	419	2	G70602	hypothetical prote
1146	49	10.6	160	2	S73261	plastoquinol-plast	1219	49	10.6	425	2	A64977	hypothetical prote
1147	49	10.6	163	2	D71062	hypothetical prote	1220	49	10.6	429	2	B87299	transporter, proba
1148	49	10.6	166	2	D82909	hypothetical prote	1221	49	10.6	431	1	E70699	probable pKNA prot
1149	49	10.6	167	2	T11439	NADH2 dehydrogenas	1222	49	10.6	439	2	D72716	hypothetical prote
1150	49	10.6	167	2	B71553	hypothetical prote	1223	49	10.6	441	2	B82023	probable membrane-
1151	49	10.6	167	2	AE3204	hypothetical prote	1224	49	10.6	444	2	T24076	hypothetical prote
1152	49	10.6	169	2	B75490	hypothetical prote	1225	49	10.6	448	2	A70398	cell division prot
1153	49	10.6	170	2	H71937	3-dehydroquinat d	1226	49	10.6	450	2	E69934	conserved hypothet
1154	49	10.6	170	2	F90050	hypothetical prote	1227	49	10.6	458	2	AC1173	amino acid transpo
1155	49	10.6	172	2	T32259	hypothetical prote	1228	49	10.6	463	2	AD1530	amino acid transpo
1156	49	10.6	174	2	E90617	NADH dehydrogenase	1229	49	10.6	463	2	C86042	probable transport
1157	49	10.6	179	1	ERAD34	early E3 20.1K gly	1230	49	10.6	463	2	B91195	probable transport
1158	49	10.6	181	2	JX0247	serine proteinase	1231	49	10.6	463	2	H65166	probable transport
1159	49	10.6	185	2	T41299	hypothetical metal	1232	49	10.6	466	2	H69822	sodium-glutamate s
1160	49	10.6	195	2	AF2690	conserved hypothet	1233	49	10.6	466	2	G72603	nitrate reductase
1161	49	10.6	195	2	B97472	hypothetical prote	1234	49	10.6	469	1	AJECQ	glutamate-ammonia
1162	49	10.6	196	2	T49023	hypothetical prote	1235	49	10.6	469	2	A83356	hypothetical prote
1163	49	10.6	196	2	G87510	hypothetical prote	1236	49	10.6	469	2	G86074	glutamine syntheta
1164	49	10.6	203	2	E72345	endopeptidase Clp	1237	49	10.6	469	2	H91227	glutamine syntheta
1165	49	10.6	203	2	T32745	hypothetical prote	1238	49	10.6	473	2	T07548	photosystem II chl
1166	49	10.6	205	2	T14744	hypothetical prote	1239	49	10.6	475	2	T36342	probable glutamate
1167	49	10.6	207	2	D75341	conserved hypothet	1240	49	10.6	475	2	T06061	cellulase (EC 3.2.
1168	49	10.6	212	2	AC0074	probable tellurium	1241	49	10.6	476	2	H96802	probable amino aci
1169	49	10.6	217	2	B90765	hypothetical prote	1242	49	10.6	485	2	G65051	phosphotransferase
1170	49	10.6	224	2	AG1795	hypothetical prote	1243	49	10.6	485	2	C91075	hypothetical prote
1171	49	10.6	236	2	B81406	hypothetical prote	1244	49	10.6	485	2	B85920	hypothetical prote
1172	49	10.6	244	2	S07398	gamma-gliadin B pr	1245	49	10.6	491	2	B71957	ATP-dependent RNA
1173	49	10.6	255	4	S31866	Ig gamma-1 chain C	1246	49	10.6	492	2	G64550	uroporphyrinogen-I
1174	49	10.6	262	2	T48346	hypothetical prote	1247	49	10.6	493	2	A11224	uroporphyrinogen-I
1175	49	10.6	263	2	AB2559	transposase all806	1248	49	10.6	493	2	AC1578	T-cell surface gly
1176	49	10.6	276	2	S73410	hypothetical prote	1249	49	10.6	495	1	A26396	probable transcrip
1177	49	10.6	287	2	E83928	transcription regu	1250	49	10.6	496	2	F83124	LAR1 protein - hum
1178	49	10.6	288	2	AH0247	probable binding-p	1251	49	10.6	507	2	JG0165	cytochrome-c hum
1179	49	10.6	300	2	G75436	conserved hypothet	1252	49	10.6	510	2	S55124	probable membrane
1180	49	10.6	308	1	QRECHB	chemotaxis protein	1253	49	10.6	516	2	C58892	cytochrome-c oxida
1181	49	10.6	308	2	C85802	hypothetical prote	1254	49	10.6	516	2	T09949	cytochrome-c oxida
1182	49	10.6	308	2	G90953	chemotaxis protein	1255	49	10.6	522	1	IKEC1	colicin E1 - Esche
1183	49	10.6	308	2	H82936	hpr serine/threoni	1256	49	10.6	526	2	E65024	Hydrogenase-4 comp
1184	49	10.6	312	2	F87335	conserved hypothet	1257	49	10.6	535	2	D96586	hypothetical prote
1185	49	10.6	322	2	AI2871	homoserine kinase	1258	49	10.6	542	2	C70732	probable integral
1186	49	10.6	322	2	G97453	homoserine kinase	1259	49	10.6	553	1	H70786	probable dihydroli
1187	49	10.6	334	1	JC4280	carboxyl reductase	1260	49	10.6	555	2	S27163	alpha,alpha-trehali
1188	49	10.6	334	2	T16772	hypothetical prote	1261	49	10.6	557	2	AE3040	alpha,alpha-trehali
1189	49	10.6	335	2	B87448	arginine N-succiny	1262	49	10.6	563	2	G98245	hutu gene homolog
1190	49	10.6	335	2	T40292	glyceraldehyde 3-p	1263	49	10.6	573	2	S28901	glutamate transpor
1191	49	10.6	337	1	QOECH3	probable dehydroge	1264	49	10.6	582	2	S22195	bps2 protein - Des
1192	49	10.6	337	2	C91029	probable PTS syste	1265	49	10.6	586	2	PC6006	scaffolding protei
1193	49	10.6	337	2	D85873	probable PTS syste	1266	49	10.6	597	2	S51212	BAK5 protein - bov
1194	49	10.6	345	2	T28026	hypothetical prote	1267	49	10.6	602	2	E70067	conserved hypothet
1195	49	10.6	349	2	C86662	hypothetical prote	1268	49	10.6	605	2	D83007	regulatory protein
1196	49	10.6	352	2	A43113	chemokine (C-C) re	1269	49	10.6	616	2	AG2957	hypothetical prote
1197	49	10.6	353	2	H88939	protein C05E4.13 [1270	49	10.6	616	2	G98325	probable c4-dicarb

979	50	10.8	606	2	S57552	hypothetical prote	1052	49.5	10.7	400	2	T46383	hypothetical prote
980	50	10.8	613	2	A56031	potassium channel	1053	49.5	10.7	401	2	D83022	hypothetical prote
981	50	10.8	610	2	E86194	hypothetical prote	1054	49.5	10.7	403	2	T09322	DNA polymerase pro
982	50	10.8	700	2	B81266	DNA topoisomerase	1055	49.5	10.7	424	2	D75330	probable beta-lact
983	50	10.8	749	1	B39898	phospholipase A2 (1056	49.5	10.7	427	2	A49518	kallistatin precu
984	50	10.8	756	2	C46882	hypothetical prote	1057	49.5	10.7	430	1	S32570	malc protein - Sur
985	50	10.8	789	2	A82688	Na+/H+ antiporter	1058	49.5	10.7	432	2	A81356	hypothetical prote
986	50	10.8	789	2	H97469	probable NADH dehy	1059	49.5	10.7	430	2	A81726	hypothetical prote
987	50	10.8	810	1	F2WMBB	2a protein - broad	1060	49.5	10.7	432	2	H64383	probable sugar tra
988	50	10.8	828	2	JCS807	trp3 protein - rat	1061	49.5	10.7	443	2	A80309	hypothetical prote
989	50	10.8	835	2	F70363	cation transportin	1062	49.5	10.7	469	2	T34645	probable Rieske ir
990	50	10.8	836	2	C97525	clpA protein (Auj22	1063	49.5	10.7	469	2	S74825	hypothetical prote
991	50	10.8	836	2	AD2744	ATP-dependent Clp	1064	49.5	10.7	476	1	VMUT4R	variant surface gl
992	50	10.8	876	2	T07101	lipoxigenase (EC 1	1065	49.5	10.7	476	2	B86829	multidrug transpor
993	50	10.8	993	2	F97717	hypothetical prote	1066	49.5	10.7	478	2	T33942	hypothetical prote
994	50	10.8	1015	2	T15830	hypothetical prote	1067	49.5	10.7	502	2	T26256	hypothetical prote
995	50	10.8	1021	2	A86421	Receptor-like seri	1068	49.5	10.7	505	2	G90419	metabolite permeas
996	50	10.8	1022	2	F87635	AcxB/AcrD/AcrF fam	1069	49.5	10.7	508	2	H86474	hypothetical prote
997	50	10.8	1277	2	T14152	synaptic scaffoldi	1070	49.5	10.7	514	2	F87592	hypothetical prote
998	50	10.8	1338	2	T40993	protein kinase cek	1071	49.5	10.7	524	2	F85429	actin interacting
999	50	10.8	1381	2	T31083	paranodin - rat	1072	49.5	10.7	538	2	T40298	membrane transport
1000	50	10.8	1479	2	T42710	mannose receptor,	1073	49.5	10.7	538	2	A83018	probable sodium/hy
1001	50	10.8	1498	2	B97355	DNA segregation At	1074	49.5	10.7	552	2	A51027	L-ascorbate oxidas
1002	50	10.8	1505	2	S26765	genome polyprotein	1075	49.5	10.7	553	2	B90153	2-isopropylmalate
1003	50	10.8	1524	2	S68553	surface layer prot	1076	49.5	10.7	556	2	T46842	K+-transporting At
1004	50	10.8	1526	2	A95528	protein F27J15.14	1077	49.5	10.7	557	2	H97351	K+-transporting At
1005	50	10.8	1687	2	S41742	calcium channel al	1078	49.5	10.7	559	2	C87307	hypothetical prote
1006	50	10.8	2109	2	T31352	hypothetical prote	1079	49.5	10.7	566	2	B82173	probable ABC trans
1007	50	10.8	2819	2	A90551	conserved hypotet	1080	49.5	10.7	579	2	S11027	L-ascorbate oxidas
1008	49.5	10.7	63	2	B90031	hypothetical prote	1081	49.5	10.7	583	2	T48473	amino acid transpo
1009	49.5	10.7	119	2	PH1544	Ig H chain V regio	1082	49.5	10.7	583	2	E83794	ABC transporter (A
1010	49.5	10.7	130	2	AD2901	hypothetical prote	1083	49.5	10.7	586	1	E89314	replication licens
1011	49.5	10.7	130	2	S67024	probable membrane	1084	49.5	10.7	660	2	B97853	NADH2 dehydrogenas
1012	49.5	10.7	150	2	F87507	conserved hypotet	1085	49.5	10.7	686	2	E71895	probable heavy-met
1013	49.5	10.7	160	2	C35542	ribosomal protein	1086	49.5	10.7	697	2	T13670	NADH2 dehydrogenas
1014	49.5	10.7	165	2	F97676	succinate dehydrog	1087	49.5	10.7	698	2	T12625	NADH2 dehydrogenas
1015	49.5	10.7	165	2	S50195	oleosin - rape	1088	49.5	10.7	699	2	T12673	NADH2 dehydrogenas
1016	49.5	10.7	171	2	S22194	hypothetical prote	1089	49.5	10.7	700	2	T23629	hypothetical prote
1017	49.5	10.7	172	2	I38644	apxIC protein - Ac	1090	49.5	10.7	701	2	T13056	NADH2 dehydrogenas
1018	49.5	10.7	197	2	AB2056	hypothetical prote	1091	49.5	10.7	701	2	T13587	NADH2 dehydrogenas
1019	49.5	10.7	214	2	B83881	siderophore (surfa	1092	49.5	10.7	702	2	T13058	NADH2 dehydrogenas
1020	49.5	10.7	218	2	AC1253	glycine betaine/ca	1093	49.5	10.7	702	2	T12624	NADH2 dehydrogenas
1021	49.5	10.7	218	2	A11615	glycine betaine/ca	1094	49.5	10.7	702	2	T13409	NADH2 dehydrogenas
1022	49.5	10.7	226	2	B87449	cell division prot	1095	49.5	10.7	703	2	T13074	NADH2 dehydrogenas
1023	49.5	10.7	244	2	E84885	hypothetical prote	1096	49.5	10.7	703	2	T13696	NADH2 dehydrogenas
1024	49.5	10.7	251	2	AF2281	hypothetical prote	1097	49.5	10.7	706	2	T12748	NADH2 dehydrogenas
1025	49.5	10.7	252	1	A34702	amphiregulin precu	1098	49.5	10.7	721	2	F82198	probable toxin sec
1026	49.5	10.7	255	2	B81302	probable membrane	1099	49.5	10.7	732	2	A83481	NADH2 dehydrogenas
1027	49.5	10.7	275	2	H90251	maltose transport	1100	49.5	10.7	734	1	DRR2N5	NADH2 dehydrogenas
1028	49.5	10.7	294	2	B83040	ribosomal protein	1101	49.5	10.7	738	2	S58612	NADH2 dehydrogenas
1029	49.5	10.7	295	2	T04483	probable ring fing	1102	49.5	10.7	740	2	B84741	hypothetical prote
1030	49.5	10.7	301	1	S10456	cytochrome c-type	1103	49.5	10.7	745	2	B84673	hypothetical prote
1031	49.5	10.7	302	2	F83392	hypothetical prote	1104	49.5	10.7	753	2	F69338	pyruvate, water di
1032	49.5	10.7	305	2	A10847	iron transport pro	1105	49.5	10.7	770	2	B56695	transducin-like en
1033	49.5	10.7	313	2	AH1672	malonyl CoA-acyl c	1106	49.5	10.7	776	2	S45495	isp4 protein - fis
1034	49.5	10.7	315	2	B98226	hypothetical prote	1107	49.5	10.7	788	1	I59282	diacylglycerol kin
1035	49.5	10.7	315	2	AF3060	conserved hypotet	1108	49.5	10.7	795	2	D82225	phenylalanyl-tRNA
1036	49.5	10.7	327	2	T21614	hypothetical prote	1109	49.5	10.7	822	2	T25866	hypothetical prote
1037	49.5	10.7	328	2	AD1916	alcohol dehydrogen	1110	49.5	10.7	826	2	AC0086	outer membrane udi
1038	49.5	10.7	330	2	H75353	probable nosx prot	1111	49.5	10.7	850	2	JCS700	ErbB kinase activa
1039	49.5	10.7	332	2	T33799	hypothetical prote	1112	49.5	10.7	875	2	T12794	hypothetical yomG
1040	49.5	10.7	334	2	T23444	hypothetical prote	1113	49.5	10.7	888	2	A54280	cell differentia
1041	49.5	10.7	341	2	B98304	probable oligopept	1114	49.5	10.7	914	1	JN0550	iodide peroxidase
1042	49.5	10.7	342	2	AB2979	hypothetical prote	1115	49.5	10.7	945	2	S77052	cation-transportin
1043	49.5	10.7	348	2	B48435	cysteine proteinas	1116	49.5	10.7	1039	2	T38447	tetratricopeptide
1044	49.5	10.7	360	2	B87286	conserved hypotet	1117	49.5	10.7	1069	2	D85383	hypothetical prote
1045	49.5	10.7	367	1	C69500	group II decarboxy	1118	49.5	10.7	1084	2	T15616	hypothetical prote
1046	49.5	10.7	368	1	QQBEHG	early nuclear anti	1119	49.5	10.7	1121	2	JC7329	WD-repeat protein
1047	49.5	10.7	372	1	D69442	conserved hypotet	1120	49.5	10.7	1132	2	T31107	telomerase reverse
1048	49.5	10.7	374	1	I39857	spore germination	1121	49.5	10.7	1163	2	A56097	arylphorin-binding
1049	49.5	10.7	374	2	T21513	hypothetical prote	1122	49.5	10.7	1195	2	S76592	5-methyltetrahydro
1050	49.5	10.7	380	1	TAGB	actinidin-(EC 3.4	1123	49.5	10.7	1354	2	AG0538	Rhs-family protein
1051	49.5	10.7	391	2	T43987	pp41, pol processi	1124	49.5	10.7	1461	2	E90696	hypothetical prote

833	50.5	11.0	442	2	S56057	heavy metal ion re	906	50	10.8	214	2	T10737	extensin-like cell
834	50.5	11.0	448	2	A83775	hypothetical prote	907	50	10.8	216	2	A11441	hypothetical prote
835	50.5	11.0	460	2	G85525	probable deaminase	908	50	10.8	219	2	T38019	uracil phosphorib
836	50.5	11.0	460	2	E96765	probable deaminase	909	50	10.8	232	2	S29001	G protein-coupled
837	50.5	11.0	470	2	T20851	hypothetical prote	910	50	10.8	236	2	T32473	hypothetical prote
838	50.5	11.0	471	2	D83546	probable amino aci	911	50	10.8	238	2	B64509	hypothetical prote
839	50.5	11.0	474	1	JH0790	lipoprotein lipase	912	50	10.8	250	2	S51206	cruxrhodopsin-1 -
840	50.5	11.0	507	2	T27627	hypothetical prote	913	50	10.8	255	2	A71351	probable cobalt AB
841	50.5	11.0	509	2	G81929	probable iron-upta	914	50	10.8	256	2	A81277	probable oxidoredu
842	50.5	11.0	510	2	T20850	hypothetical prote	915	50	10.8	259	2	C75151	oxidoreductase PAB
843	50.5	11.0	515	2	G75267	ABC transporter, p	916	50	10.8	265	2	D81315	hypothetical prote
844	50.5	11.0	517	2	S21042	cytochrome-c oxida	917	50	10.8	265	2	G73460	hypothetical prote
845	50.5	11.0	518	2	S34565	gene G protein - h	918	50	10.8	268	2	C83369	probable binding p
846	50.5	11.0	518	2	F70831	probable PPE prote	919	50	10.8	274	2	E75614	conserved hypothet
847	50.5	11.0	520	2	AD2383	Na+/H+-exchanging	920	50	10.8	293	2	T36063	probable integral
848	50.5	11.0	526	2	G83436	hypothetical prote	921	50	10.8	295	2	B85787	probable transposa
849	50.5	11.0	529	1	YRHU1	monophenol monooxy	922	50	10.8	295	2	T00315	transposase - Esch
850	50.5	11.0	543	2	T37570	WD repeat protein	923	50	10.8	296	2	I67971	transposase - Esch
851	50.5	11.0	543	2	S65462	glucose transport	924	50	10.8	296	2	D90398	conserved hypothet
852	50.5	11.0	544	2	AD1979	permease protein o	925	50	10.8	299	2	S50803	hypothetical prote
853	50.5	11.0	545	2	AC1914	hypothetical prote	926	50	10.8	299	2	A72596	hypothetical prote
854	50.5	11.0	546	2	B40407	sterol carrier pro	927	50	10.8	304	2	A72596	hypothetical prote
855	50.5	11.0	563	2	S32156	mandelonitrile lya	928	50	10.8	314	2	S22928	ubiquinol-cytochro
856	50.5	11.0	577	2	T52608	probable nitrate t	929	50	10.8	317	2	B87666	pectinesterase (EC
857	50.5	11.0	584	2	S40013	hypothetical prote	930	50	10.8	332	2	C87426	homoserine kinase
858	50.5	11.0	586	2	F84663	probable nitrate t	931	50	10.8	332	2	C84061	cysteine synthase
859	50.5	11.0	595	2	AH2718	aspartyl-tRNA synt	932	50	10.8	333	2	T36036	ferrichrome ABC tr
860	50.5	11.0	595	2	D97500	aspartyl-tRNA syn	933	50	10.8	337	2	AG0802	probable integral
861	50.5	11.0	608	2	T56192	hypothetical prote	934	50	10.8	341	2	D48435	probable semialdeh
862	50.5	11.0	684	2	T25603	hypothetical prote	935	50	10.8	348	2	E86818	cysteine proteinase
863	50.5	11.0	688	2	H96681	protein Flt22.10 {	936	50	10.8	357	2	D83685	dehydrogenase [imp
864	50.5	11.0	704	2	F87706	prolyl oligopeptid	937	50	10.8	357	2	T09261	nicotinate-nucleot
865	50.5	11.0	712	2	AD2721	H+ translocating p	938	50	10.8	372	2	S20056	JUN kinase-activat
866	50.5	11.0	714	2	H97502	h+ translocating p	939	50	10.8	375	2	T25089	para-hydroxybenzoa
867	50.5	11.0	731	2	E82922	phosphate transpor	940	50	10.8	380	2	A71390	ubiquinol-cytochro
868	50.5	11.0	736	2	C82821	bacteriophytochrom	941	50	10.8	388	2	D69468	ammonium transport
869	50.5	11.0	745	2	C97599	cyanobacterial phy	942	50	10.8	388	2	AF0183	probable exported
870	50.5	11.0	819	2	F87708	cell division proc	943	50	10.8	393	2	S61659	KTR1 protein - yea
871	50.5	11.0	827	2	A95877	hypothetical prote	944	50	10.8	397	2	E91296	probable thymidine
872	50.5	11.0	908	2	A10327	two-component regu	945	50	10.8	407	2	F70318	hypothetical prote
873	50.5	11.0	942	1	JQ1674	protein kinase TMK	946	50	10.8	414	1	E70708	hypothetical prote
874	50.5	11.0	962	2	T05945	hypothetical prote	947	50	10.8	420	2	A12379	cytochrome P450 Rv
875	50.5	11.0	1163	1	RWHU1C	cell surface glyco	948	50	10.8	434	2	A12379	conserved hypothet
876	50.5	11.0	1188	2	T20333	hypothetical prote	949	50	10.8	435	2	G82907	hypothetical prote
877	50.5	11.0	1265	2	T47626	structural mainten	950	50	10.8	440	1	S56606	D-alanyl-D-alanine
878	50.5	11.0	1317	2	T03748	apoptosis associat	951	50	10.8	440	1	G86137	thymidine phosphor
879	50.5	11.0	1345	2	T44204	capsid protein U57	952	50	10.8	449	2	H69862	hypothetical prote
880	50.5	11.0	1345	2	T44017	major capsid prote	953	50	10.8	457	1	A28468	Na+-transporting A
881	50.5	11.0	1400	2	B70963	hypothetical prote	954	50	10.8	457	1	A28468	chromogranin A pre
882	50.5	11.0	1447	1	VGIHE3	hypothetical prote	955	50	10.8	457	2	A53669	streptogrin C (E
883	50.5	11.0	1447	1	VGIHE2	E2 glycoprotein pr	956	50	10.8	460	2	JL0145	interleukin-6 rece
884	50.5	11.0	1449	1	A43573	E2 glycoprotein pr	957	50	10.8	473	1	F2R244	photosystem II chl
885	50.5	11.0	1449	1	VGIHFS	E2 glycoprotein pr	958	50	10.8	473	1	F2SP44	photosystem II chl
886	50.5	11.0	1577	2	T15851	hypothetical prote	959	50	10.8	473	2	T08998	photosystem II pro
887	50.5	11.0	1672	2	C81675	polymorphic membra	960	50	10.8	476	2	AC2306	hypothetical prote
888	50.5	11.0	1921	2	T13827	kinesin-73 - fruit	961	50	10.8	489	2	A11639	multidrug-efflux t
889	50	10.8	89	2	H83795	hypothetical prote	962	50	10.8	494	2	C70940	probable cobQ prot
890	50	10.8	100	2	A12298	cobalt transport p	963	50	10.8	498	2	F98149	hypothetical prote
891	50	10.8	102	2	A75417	hypothetical prote	964	50	10.8	514	2	C49507	potassium channel
892	50	10.8	121	2	B72546	hypothetical prote	965	50	10.8	516	2	S39686	monophenol monooxy
893	50	10.8	138	2	JC1342	phospholipase A2 (966	50	10.8	532	2	JC1392	hypothetical prote
894	50	10.8	147	2	S70109	hypothetical prote	967	50	10.8	533	2	AE3138	probable biotin-de
895	50	10.8	150	2	G72660	hypothetical prote	968	50	10.8	538	2	C83284	hypothetical prote
896	50	10.8	170	2	B86942	hypothetical prote	969	50	10.8	538	2	C86976	PPE-family protein
897	50	10.8	175	2	T11179	NADH2 dehydrogenas	970	50	10.8	539	2	C83758	cephalosporin acyl
898	50	10.8	175	2	AE1149	hypothetical prote	971	50	10.8	542	2	S50361	probable membrane
899	50	10.8	186	2	E82625	outer membrane pro	972	50	10.8	545	2	T18694	hypothetical prote
900	50	10.8	195	2	T39603	BAG-family molecul	973	50	10.8	545	2	T39499	conserved hypothet
901	50	10.8	203	2	D81934	probable periplasm	974	50	10.8	573	2	D83440	probable sulfate t
902	50	10.8	203	2	F81171	cryptic protein NM	975	50	10.8	588	2	T25248	hypothetical prote
903	50	10.8	211	2	A47686	bacteriorhodopsin-	976	50	10.8	598	2	S66669	potassium channel
904	50	10.8	211	2	AC0268	probable exported	977	50	10.8	602	2	A49507	potassium channel
905	50	10.8	213	2	G75521	ABC transporter, A	978	50	10.8	602	2	JH0166	potassium voltage-

687	51	11.1	279	2	T22051	hypothetical prote	760	50.5	11.0	173	2	S59864	TRAP-like protein
688	51	11.1	282	2	E64063	hypothetical prote	761	50.5	11.0	201	1	IMPSB	immunity protein -
689	51	11.1	285	2	A41025	asparaginopeptin I	762	50.5	11.0	204	2	E83036	hypothetical prote
690	51	11.1	282	2	T15498	hypothetical prote	763	50.5	11.0	208	2	F71314	probable transcrip
691	51	11.1	295	2	F90938	hypothetical prote	764	50.5	11.0	217	2	I51062	MHC class II beta
692	51	11.1	295	2	B85664	transposase for IS	765	50.5	11.0	224	2	T34686	probable integral
693	51	11.1	295	2	D90801	hypothetical prote	766	50.5	11.0	227	2	T12797	immunity protein d
694	51	11.1	295	2	B85613	probable transposa	767	50.5	11.0	228	2	C28551	hypothetical prote
695	51	11.1	309	2	AF0746	motility protein B	768	50.5	11.0	231	2	H81698	hypothetical prote
696	51	11.1	321	1	A55090	cathepsin O (EC 3.	769	50.5	11.0	233	2	JH0372	42K surface glycop
697	51	11.1	328	1	S64306	hypothetical prote	770	50.5	11.0	234	2	E95360	hypothetical prote
698	51	11.1	345	2	AG0645	spermidine/putresc	771	50.5	11.0	240	1	TOEC34	transposase - Esch
699	51	11.1	355	2	E96785	protein F10A5_28 [772	50.5	11.0	247	2	I51060	MHC class II beta
700	51	11.1	357	2	A71523	probable chorismat	773	50.5	11.0	247	2	I51059	MHC class II beta
701	51	11.1	361	2	A45211	prostaglandin E re	774	50.5	11.0	249	2	S75671	hypothetical prote
702	51	11.1	362	2	A35058	prostaglandin F2-a	775	50.5	11.0	249	2	H95256	ABC transporter, p
703	51	11.1	364	2	S65009	prostaglandin E re	776	50.5	11.0	250	2	T09160	proteasome subunit
704	51	11.1	365	2	A42414	prostaglandin E re	777	50.5	11.0	252	2	F70711	probable membranep
705	51	11.1	372	2	S75587	H+/Ca2+ exchanging	778	50.5	11.0	253	2	A98122	hypothetical prote
706	51	11.1	375	2	T03256	GTP-binding protei	779	50.5	11.0	255	2	JN0829	3alpha-hydroxyster
707	51	11.1	377	2	T04086	GTP binding protei	780	50.5	11.0	258	2	A69805	hypothetical prote
708	51	11.1	377	2	T16985	GTP-binding protei	781	50.5	11.0	260	2	F82954	probable short-cha
709	51	11.1	379	2	AB2423	hypothetical prote	782	50.5	11.0	264	2	D87504	hypothetical prote
710	51	11.1	384	2	A69622	ferrichrome ABC tr	783	50.5	11.0	286	2	E86844	shikimate 5-dehydr
711	51	11.1	394	2	B85535	probable transport	784	50.5	11.0	288	2	F85818	hypothetical prote
712	51	11.1	394	2	F90684	probable transport	785	50.5	11.0	293	2	A83623	hypothetical prote
713	51	11.1	402	2	B82491	NupC family protei	786	50.5	11.0	296	2	A85841	probable transposa
714	51	11.1	404	2	T39270	conserved hypothet	787	50.5	11.0	296	2	D91284	hypothetical prote
715	51	11.1	409	2	G90491	conserved hypothet	788	50.5	11.0	296	2	F90868	hypothetical prote
716	51	11.1	416	2	T14554	calreticulin - bee	789	50.5	11.0	296	2	D90995	hypothetical prote
717	51	11.1	418	2	S31124	hypothetical prote	790	50.5	11.0	296	2	E91020	hypothetical prote
718	51	11.1	421	2	B82062	conserved hypothet	791	50.5	11.0	296	2	A91132	hypothetical prote
719	51	11.1	423	2	AB0054	probable Na+ depen	792	50.5	11.0	296	2	F91111	hypothetical prote
720	51	11.1	435	2	E71350	probable aspartate	793	50.5	11.0	296	2	G90998	hypothetical prote
721	51	11.1	439	2	S58327	cobalt accumulatio	794	50.5	11.0	296	2	T00240	transposase - Esch
722	51	11.1	439	2	T18898	hypothetical prote	795	50.5	11.0	296	2	B90837	hypothetical prote
723	51	11.1	440	2	AD1073	thymidine phosphor	796	50.5	11.0	296	2	C91065	hypothetical prote
724	51	11.1	449	2	C86496	hypothetical prote	797	50.5	11.0	296	2	H90779	hypothetical prote
725	51	11.1	449	2	D72127	hypothetical prote	798	50.5	11.0	296	2	C90906	hypothetical prote
726	51	11.1	449	2	A81544	hypothetical prote	799	50.5	11.0	296	2	A99972	hypothetical prote
727	51	11.1	450	2	AB1420	PTS cellobiose-spe	800	50.5	11.0	297	2	T09542	endonuclease G (SC
728	51	11.1	450	2	AC1795	PTS cellobiose-spe	801	50.5	11.0	297	2	T45436	hypothetical membr
729	51	11.1	458	1	YTB5Y8	tetracycline resis	802	50.5	11.0	302	2	S02728	actinidin (EC 3.4
730	51	11.1	460	2	S06469	photosystem II chl	803	50.5	11.0	302	2	S60955	probable membrane
731	51	11.1	466	2	E84132	aminopeptidase BH3	804	50.5	11.0	313	2	AH1300	malonyl CoA-acyl c
732	51	11.1	468	2	A69468	ammonium transport	805	50.5	11.0	314	2	F86928	34 kDa antigen [im
733	51	11.1	485	2	A72006	arginine/ornithine	806	50.5	11.0	317	2	T27994	hypothetical prote
734	51	11.1	514	2	A96671	Ammonium transport	807	50.5	11.0	324	2	A86839	conserved hypothet
735	51	11.1	516	2	T09859	cytochrome-c oxida	808	50.5	11.0	327	2	S61982	probable membrane
736	51	11.1	525	2	T00459	hypothetical prote	809	50.5	11.0	332	2	S77386	nitrate transport
737	51	11.1	528	2	T25583	hypothetical prote	810	50.5	11.0	346	2	C71390	NADH2 dehydrogenas
738	51	11.1	531	2	T12406	cytochrome-c oxida	811	50.5	11.0	351	2	A69808	H+/Ca2+ exchanger
739	51	11.1	560	2	T51485	sugar transporter-	812	50.5	11.0	355	1	BVECMG	UDP-N-acetylglucos
740	51	11.1	562	2	T07611	aconitate hydratase	813	50.5	11.0	355	2	F85491	hypothetical prote
741	51	11.1	635	1	A64162	cytochrome c-type	814	50.5	11.0	355	2	F90640	hypothetical prote
742	51	11.1	639	2	JQ0607	glucan 1,4-alpha-g	815	50.5	11.0	361	2	F87286	cation efflux fani
743	51	11.1	699	2	A68602	unknown protein [i	816	50.5	11.0	362	2	JC7559	sphingosine 1-phos
744	51	11.1	745	1	A70458	phosphoribosylform	817	50.5	11.0	364	2	H70776	hypothetical prote
745	51	11.1	749	1	A93329	phospholipase A2 (818	50.5	11.0	377	2	B53044	geranylgeranyl-dip
746	51	11.1	750	2	S37403	transcription fact	819	50.5	11.0	379	2	T45768	protein phosphatas
747	51	11.1	774	2	T50308	probable tranelati	820	50.5	11.0	382	2	H90500	glycolate oxidase
748	51	11.1	778	2	E97224	ATP-dependent Lon	821	50.5	11.0	398	2	S75202	hypothetical prote
749	51	11.1	854	2	T23837	hypothetical prote	822	50.5	11.0	399	2	T26257	hypothetical prote
750	51	11.1	862	2	T46289	hypothetical prote	823	50.5	11.0	406	2	T27947	hypothetical prote
751	51	11.1	873	2	T16282	hypothetical prote	824	50.5	11.0	407	2	E70309	hypothetical prote
752	51	11.1	887	2	T01113	translation initia	825	50.5	11.0	408	2	T29949	hypothetical prote
753	51	11.1	967	2	A30325	membrane alanyl am	826	50.5	11.0	410	2	JC7584	basic helix-loop-h
754	51	11.1	1075	2	D70568	hypothetical prote	827	50.5	11.0	411	2	AG3003	conserved hypothet
755	51	11.1	1325	2	A64905	ydek protein - Bsc	828	50.5	11.0	411	2	B98280	hypothetical prote
756	51	11.1	1790	1	D73772	vitellogenin precu	829	50.5	11.0	421	2	D70868	probable lipQ prot
757	50.5	11.0	137	2	D75337	hypothetical prote	830	50.5	11.0	424	2	A71846	glycinamide ribonu
758	50.5	11.0	141	2	E72580	hypothetical prote	831	50.5	11.0	424	2	B64672	glycinamide ribonu
759	50.5	11.0	155	2	T22027	hypothetical prote	832	50.5	11.0	441	2	AF0411	probable chloride

541	52	11.3	417	2	E69804	multidrug resistanc	614	51.5	11.2	410	2	S45894	regulatory protein
542	52	11.3	457	2	S39079	puff C-8 protein -	615	51.5	11.2	429	2	F87038	probable membrane
543	52	11.3	469	2	D81017	chloride channel p	616	51.5	11.2	438	2	A83037	probable MFS trans
544	52	11.3	470	2	D70641	hypothetical prote	617	51.5	11.2	450	2	C96704	unknown protein, 2
545	52	11.3	491	2	S75449	hypothetical prote	618	51.5	11.2	451	2	F75177	tryptophan synthas
546	52	11.3	502	2	G87433	conserved hypothet	619	51.5	11.2	474	1	A40570	lipoprotein lipase
547	52	11.3	502	2	T29729	hypothetical prote	620	51.5	11.2	478	1	C42790	cystathionine beta
548	52	11.3	526	2	H85891	hydrogenase 4 memb	621	51.5	11.2	478	2	T30763	hypothetical prote
549	52	11.3	526	2	D91047	hydrogenase 4 memb	622	51.5	11.2	478	2	T32476	probable protein-t
550	52	11.3	530	2	D87255	apolipoprotein N-a	623	51.5	11.2	481	2	B82130	pyruvate kinase II
551	52	11.3	534	2	T27054	hypothetical prote	624	51.5	11.2	493	2	T21445	hypothetical prote
552	52	11.3	544	2	T17422	halogenase-like pr	625	51.5	11.2	509	2	G82409	glyceraldehyde 3-p
553	52	11.3	548	2	C82698	electron transfer	626	51.5	11.2	513	2	T34546	hypothetical prote
554	52	11.3	553	2	S75892	probable glycerol-	627	51.5	11.2	525	2	A70735	probable guaA prot
555	52	11.3	567	2	H87370	major facilitator	628	51.5	11.2	531	2	D96965	PTS system, arbuti
556	52	11.3	573	2	A33533	cell surface glyco	629	51.5	11.2	534	1	JU0274	cell fusion glycop
557	52	11.3	579	2	A64100	inner membrane cop	630	51.5	11.2	536	2	D81700	CTP synthase TC045
558	52	11.3	635	2	H69626	PTS fructose-speci	631	51.5	11.2	536	2	F85697	hypothetical prote
559	52	11.3	706	2	H81943	probable polyribon	632	51.5	11.2	536	2	D64865	probable Na+/H+-ex
560	52	11.3	707	2	C81161	polynucleotide	633	51.5	11.2	536	2	F90839	hypothetical prote
561	52	11.3	733	2	S37876	hypothetical prote	634	51.5	11.2	540	1	JU0470	site-specific DNA-
562	52	11.3	738	2	S37876	glutamine-rich pro	635	51.5	11.2	541	1	A70022	multidrug-efflux t
563	52	11.3	773	2	AH2061	hypothetical prote	636	51.5	11.2	541	2	JN0511	heat shock protein
564	52	11.3	823	2	A96737	hypothetical prote	637	51.5	11.2	547	2	T46059	MAP kinase - Arabi
565	52	11.3	840	2	T21333	hypothetical prote	638	51.5	11.2	549	2	T51099	cell fusion glycop
566	52	11.3	889	2	A95156	conserved hypothet	639	51.5	11.2	550	1	E48556	conserved hypothet
567	52	11.3	878	2	D98022	conserved hypothet	640	51.5	11.2	558	2	C72391	interferon alpha r
568	52	11.3	906	2	AE2533	hypothetical prote	641	51.5	11.2	560	2	T27387	cystathionine beta
569	52	11.3	1016	2	T00375	hypothetical prote	642	51.5	11.2	561	1	A42790	probable membrane
570	52	11.3	1017	2	T37201	hypothetical prote	643	51.5	11.2	623	2	T35377	transketolase (EC
571	52	11.3	1106	2	A97647	cation efflux syst	644	51.5	11.2	666	2	AF0815	transketolase (EC
572	52	11.3	1106	2	AG2870	Acr family transpo	645	51.5	11.2	667	1	A48660	transketolase 2 is
573	52	11.3	1146	2	T09112	probable sensor ki	646	51.5	11.2	667	2	G91044	transketolase 2 is
574	52	11.3	1146	2	A82174	sensory box sensor	647	51.5	11.2	667	2	B85889	NADH2 dehydrogenas
575	52	11.3	1146	2	C97196	probable membrane	648	51.5	11.2	682	2	T12715	hypothetical prote
576	52	11.3	1957	2	S68453	sodium channel pro	649	51.5	11.2	724	2	T19601	hypothetical prote
577	52	11.3	2139	2	A44467	voltage-dependent	650	51.5	11.2	726	2	T31287	hypothetical prote
578	52	11.3	2220	2	A45290	calcium channel pr	651	51.5	11.2	763	2	A13443	Na+/H+ antiporter
579	52	11.3	3429	2	T13853	hypothetical prote	652	51.5	11.2	765	2	B52888	hypothetical prote
580	51.5	11.2	116	2	A83693	transcription regu	653	51.5	11.2	795	2	AE0705	phenylalanyl-tRNA
581	51.5	11.2	132	1	PSABA	phospholipase A2 (654	51.5	11.2	829	2	T29372	hypothetical prote
582	51.5	11.2	146	2	C72563	hypothetical prote	655	51.5	11.2	846	2	T27282	hypothetical prote
583	51.5	11.2	146	2	S42570	flavodoxin - desul	656	51.5	11.2	869	2	C56617	cfaC protein precu
584	51.5	11.2	167	2	H86784	WSP29-like phospho	657	51.5	11.2	1451	1	JQ1719	E2 glycoprotein pr
585	51.5	11.2	172	2	F75491	conserved hypothet	658	51.5	11.2	1755	2	T51532	hypothetical prote
586	51.5	11.2	206	1	I40173	orotate phosphorib	659	51.5	11.2	1784	2	T43167	sodium channel pro
587	51.5	11.2	209	2	T00733	hypothetical prote	660	51.5	11.2	2301	1	GNNYTN	genome polyprotein
588	51.5	11.2	212	1	A49436	dual specificity p	661	51.5	11.2	2303	1	GNNYTM	genome polyprotein
589	51.5	11.2	222	2	H64495	cobalamin biosynth	662	51	11.1	89	2	AH3403	hypothetical prote
590	51.5	11.2	270	2	A29934	pancreatic elastas	663	51	11.1	93	2	A86491	conserved hypothet
591	51.5	11.2	276	2	A70425	hypothetical prote	664	51	11.1	93	2	F72130	hypothetical prote
592	51.5	11.2	282	2	AC2294	hypothetical prote	665	51	11.1	95	2	AG2439	hypothetical prote
593	51.5	11.2	289	2	G97192	oligopeptide ABC-t	666	51	11.1	97	2	C75415	hypothetical prote
594	51.5	11.2	299	2	B95939	probable spermidin	667	51	11.1	106	2	A72588	conserved hypothet
595	51.5	11.2	299	2	H97884	hypothetical prote	668	51	11.1	152	2	H95153	hypothetical prote
596	51.5	11.2	312	2	B69170	UDP-N-acetylmuram	669	51	11.1	173	2	AF2518	hypothetical prote
597	51.5	11.2	313	2	S75329	hypothetical prote	670	51	11.1	188	2	T15651	hypothetical prote
598	51.5	11.2	314	2	T21971	hypothetical prote	671	51	11.1	201	2	E75039	multiple antibioti
599	51.5	11.2	319	2	T02691	glyssyl protein gl	672	51	11.1	202	2	A81441	probable orotate p
600	51.5	11.2	342	2	T16806	hypothetical prote	673	51	11.1	204	2	A82389	conserved hypothet
601	51.5	11.2	355	2	S76667	hypothetical prote	674	51	11.1	212	2	I67437	cysteine proteinas
602	51.5	11.2	364	2	G82734	acetylornithine de	675	51	11.1	221	2	S75146	hypothetical prote
603	51.5	11.2	366	2	I53488	prostaglandin F2 a	676	51	11.1	229	2	E85806	hypothetical prote
604	51.5	11.2	366	2	S51281	F2-alpha receptor	677	51	11.1	229	2	D90958	hypothetical prote
605	51.5	11.2	370	2	AH1485	fructose-specific	678	51	11.1	240	2	T02059	GRP-binding regula
606	51.5	11.2	370	2	AH1124	fructose-specific	679	51	11.1	246	2	S26826	histone H1 - maize
607	51.5	11.2	376	2	A75381	peptide ABC transp	680	51	11.1	246	2	T28166	hypothetical prote
608	51.5	11.2	380	2	D83174	probable acetylpol	681	51	11.1	261	2	A71192	probable glucose 1
609	51.5	11.2	381	2	A35300	G protein-coupled	682	51	11.1	263	2	AG2280	glutathione S-tran
610	51.5	11.2	381	2	F87553	aminotransferase,	683	51	11.1	264	2	G96978	uncharacterized co
611	51.5	11.2	382	2	G84971	ompF-like porin [i	684	51	11.1	264	2	B81229	phosphatidate cyti
612	51.5	11.2	383	2	I53870	Edg-1 orphan recep	685	51	11.1	265	2	A82000	phosphatidate cyti
613	51.5	11.2	390	2	C95954	hypothetical prote	686	51	11.1	268	2	S03328	embryonic abundant

395	53	11.5	385	2	B86024	probable membrane	468	52.5	11.4	409	2	T47644	protein phosphatas
396	53	11.5	385	2	S47733	yh1u protein precu	469	52.5	11.4	410	2	B48585	transcription fact
397	53	11.5	386	2	A26017	patatin T5 precurs	470	52.5	11.4	421	2	T35515	hypothetical prote
398	53	11.5	403	2	E69873	cell-division prot	471	52.5	11.4	422	2	JR0239	lin-10 protein - r
399	53	11.5	405	2	S61551	breast-regressing	472	52.5	11.4	422	2	E82904	hypothetical prote
400	53	11.5	409	2	F83493	probable MFS trans	473	52.5	11.4	429	2	AF0681	probable voltage g
401	53	11.5	418	2	H82087	NupC family protei	474	52.5	11.4	429	2	S30049	transcription fact
402	53	11.5	426	2	B82712	ATP-dependent Cip	475	52.5	11.4	452	2	G35356	probable oxidoredu
403	53	11.5	438	2	G87675	arylesterase-relat	476	52.5	11.4	500	2	H70629	probable AMINOPBP
404	53	11.5	447	2	H86534	hypothetical prote	477	52.5	11.4	514	2	T21286	hypothetical prote
405	53	11.5	447	2	H72089	hypothetical prote	478	52.5	11.4	523	2	S53401	probable membrane
406	53	11.5	463	2	B81580	hypothetical prote	479	52.5	11.4	533	1	YRMSCS	monophenol monooxy
407	53	11.5	469	1	AJF8QT	glutamate-ammonia	480	52.5	11.4	542	2	AH2191	hypothetical prote
408	53	11.5	469	2	A10949	glutamate-syntheta	481	52.5	11.4	542	2	AI3564	hypothetical membr
409	53	11.5	469	2	S23899	glutamate-ammonia	482	52.5	11.4	546	2	B32688	beta-galactosidase
410	53	11.5	471	2	S78347	photosystem II chl	483	52.5	11.4	549	2	G91178	cytoplasmic trehal
411	53	11.5	515	2	B84406	TRK potassium upta	484	52.5	11.4	549	2	H86024	cytoplasmic trehal
412	53	11.5	581	2	T38501	hypothetical prote	485	52.5	11.4	549	2	S47739	probable alpha,alp
413	53	11.5	586	2	T20036	hypothetical prote	486	52.5	11.4	572	2	A55676	excitatory amino a
414	53	11.5	588	2	AC2276	oligopeptide bindi	487	52.5	11.4	652	2	AI2245	thiamin biosynthes
415	53	11.5	605	2	E69153	cadmium efflux ATP	488	52.5	11.4	657	1	A64079	2',3'-cyclic-nucle
416	53	11.5	610	2	A55939	dihydrolipoamide S	489	52.5	11.4	686	2	T06700	hypothetical prote
417	53	11.5	618	2	AI3303	hypothetical prote	490	52.5	11.4	699	2	T12170	NADH2 dehydrogenas
418	53	11.5	637	2	T49099	dihydrolipoamide S	491	52.5	11.4	699	2	T12172	NADH2 dehydrogenas
419	53	11.5	653	2	A83154	probable choline t	492	52.5	11.4	699	2	T12173	phenylalanine-trNA
420	53	11.5	656	2	T52064	dnau-like protein	493	52.5	11.4	795	1	SYECFB	phenylalanine trNA
421	53	11.5	728	2	D86278	hypothetical prote	494	52.5	11.4	795	2	H85779	phenylalanine trNA
422	53	11.5	770	2	T23999	hypothetical prote	495	52.5	11.4	795	2	D90931	glucose dehydrogen
423	53	11.5	776	2	T02584	probable protein k	496	52.5	11.4	803	2	F83360	malate synthase, p
424	53	11.5	1005	2	B82969	sarcosine oxidase	497	52.5	11.4	826	2	E90289	conserved hypothet
425	53	11.5	1070	2	JC4593	protein-tyrosine k	498	52.5	11.4	883	2	AE0207	hypothetical prote
426	53	11.5	1162	2	E84431	probable Na+/H+ an	499	52.5	11.4	977	2	T41289	hypothetical prote
427	53	11.5	1176	2	E58345	protein tyrosine p	500	52.5	11.4	1011	2	T40851	hypothetical prote
428	53	11.5	1240	1	TJ0BE21	DNA-directed DNA p	501	52.5	11.4	1205	2	T18517	procollagen N-endo
429	53	11.5	1250	2	T00454	hypothetical prote	502	52.5	11.4	1225	1	S24284	E2 glycoprotein pr
430	53	11.5	1305	2	T23314	hypothetical prote	503	52.5	11.4	1225	2	A36607	E2 glycoprotein -
431	53	11.5	1326	2	B58395	secretory phosphol	504	52.5	11.4	1345	1	VCBEHG	major capsid prote
432	53	11.5	1331	2	S05011	calcium channel al	505	52.5	11.4	1453	2	S41453	spike protein - ca
433	53	11.5	1465	2	A56395	secretory phosphol	506	52.5	11.4	1541	2	T30227	pipicolate-incorpo
434	53	11.5	1529	2	T16779	hypothetical prote	507	52.5	11.4	1544	2	T29482	hypothetical prote
435	53	11.5	2143	2	JH0427	voltage-dependent	508	52.5	11.4	2285	1	G02434	DNA-directed DNA p
436	53	11.5	2166	2	S11339	calcium channel pr	509	52	11.3	119	2	D64611	hypothetical prote
437	53	11.5	2171	2	S05054	calcium channel al	510	52	11.3	122	2	F75351	hypothetical prote
438	53	11.5	2599	2	A96616	unknown protein F1	511	52	11.3	148	2	D64356	conserved hypothet
439	52.5	11.4	71	2	I50439	vitellogenin III -	512	52	11.3	160	2	G95113	regulatory protein
440	52.5	11.4	78	2	G64333	ribosomal protein	513	52	11.3	162	2	H37982	regulatory protein
441	52.5	11.4	159	2	E85360	ribosomal protein	514	52	11.3	175	2	AE1508	hypothetical prote
442	52.5	11.4	165	2	C72116	hypothetical prote	515	52	11.3	202	2	JC4635	tumor-associated L
443	52.5	11.4	210	2	A83516	probable outer mem	516	52	11.3	207	2	T45600	hypothetical prote
444	52.5	11.4	219	2	F75402	probable competenc	517	52	11.3	219	2	G97271	probable phosphogl
445	52.5	11.4	219	2	AC1881	hypothetical prote	518	52	11.3	235	2	E82173	pseudouridine synt
446	52.5	11.4	244	2	S29982	class II histocomp	519	52	11.3	238	2	C82866	conjugal transfer
447	52.5	11.4	245	2	S29980	class II histocomp	520	52	11.3	260	2	I56559	neurospain - mouse
448	52.5	11.4	256	2	S14518	chlorophyll a/b-bi	521	52	11.3	262	2	B81200	conserved hypothet
449	52.5	11.4	257	2	S29981	class II histocomp	522	52	11.3	265	2	D83761	hypothetical prote
450	52.5	11.4	285	1	A43556	homeotic protein H	523	52	11.3	291	2	B75618	chromosome partiti
451	52.5	11.4	289	2	E64330	dihydrodipicolinat	524	52	11.3	295	2	E85661	probable transposa
452	52.5	11.4	296	2	S09261	probable transposa	525	52	11.3	297	2	T47857	myb protein-like -
453	52.5	11.4	301	2	B64189	glycine cleavage s	526	52	11.3	310	2	S46239	ribosome-inactivat
454	52.5	11.4	309	2	A87564	membrane protein,	527	52	11.3	310	2	T32005	hypothetical prote
455	52.5	11.4	310	2	C39778	tagatose-6-phospha	528	52	11.3	320	2	AI2305	hypothetical prote
456	52.5	11.4	310	2	T31125	hypothetical prote	529	52	11.3	327	2	AE2608	transcription regu
457	52.5	11.4	322	2	AF1031	hypothetical prote	530	52	11.3	327	2	G97390	arac family transc
458	52.5	11.4	332	2	C72310	conserved hypothet	531	52	11.3	359	2	A43532	B-cell surface ant
459	52.5	11.4	334	2	D81217	hypothetical prote	532	52	11.3	364	2	B71139	hypothetical prote
460	52.5	11.4	344	2	T33950	hypothetical prote	533	52	11.3	372	2	B64819	probable membrane
461	52.5	11.4	342	2	C48435	cysteine proteinas	534	52	11.3	372	2	B85591	hypothetical prote
462	52.5	11.4	356	2	D84280	hypothetical prote	535	52	11.3	372	2	G90740	hypothetical prote
463	52.5	11.4	360	2	T51344	RNA helicase RH18	536	52	11.3	375	2	S47704	hypothetical 41.1K
464	52.5	11.4	367	2	A49877	prostaglandin F re	537	52	11.3	375	2	F91173	probable transport
465	52.5	11.4	377	2	C69758	amino acid transpo	538	52	11.3	375	2	F86019	probable transport
466	52.5	11.4	394	2	B86507	hypothetical prote	539	52	11.3	379	2	F83152	hypothetical prote
467	52.5	11.4	394	2	B81554	hypothetical prote	540	52	11.3	397	2	B70048	conserved hypothet

249	54.5	11.8	185	2	T51844	RING-H2 finger pro	322	54	11.7	909	2	T00009	probable primase (
250	54.5	11.8	204	2	AC1961	ATP-dependent Clp	323	54	11.7	967	2	I40889	sarcosine oxidase
251	54.5	11.8	226	2	S76020	endopeptidase Clp	324	54	11.7	993	2	A38437	probable homeotic
252	54.5	11.8	255	2	F86203	hypothetical prote	325	54	11.7	1072	2	T50949	verprolin related
253	54.5	11.8	269	2	T19947	hypothetical prote	326	54	11.7	1222	2	G72614	probable reverse g
254	54.5	11.8	276	2	AC1838	hypothetical prote	327	54	11.7	1283	2	T18939	hypothetical prote
255	54.5	11.8	282	2	PQ3176	cell fusion glycop	328	53.5	11.6	114	2	C90344	oleosin-like prote
256	54.5	11.8	296	2	F83145	probable epoxide h	329	53.5	11.6	153	2	T49895	hypothetical prote
257	54.5	11.8	296	2	A85698	transposase for IS	330	53.5	11.6	173	2	S01145	hypothetical prote
258	54.5	11.8	296	2	A99840	transposase for IS	331	53.5	11.6	211	2	G82573	CDP-diacylglycerol
259	54.5	11.8	304	2	S59965	phosphotransferase	332	53.5	11.6	225	1	CyRGE	epsilon-crystallin
260	54.5	11.8	337	2	G87487	conserved hypothet	333	53.5	11.6	269	2	D96957	uncharacterized me
261	54.5	11.8	362	2	S77244	biotin synthase [E	334	53.5	11.6	282	2	PQ0388	cell fusion glycop
262	54.5	11.8	369	2	F81722	hypothetical prote	335	53.5	11.6	296	2	C90978	IS629 transposase
263	54.5	11.8	373	2	G85355	nodulin-like prote	336	53.5	11.6	296	2	H85824	IS629 transposase
264	54.5	11.8	393	2	AB0335	cystathionine beta	337	53.5	11.6	303	2	T13598	trypsin homolog -
265	54.5	11.8	422	2	T07967	mandelonitrile lyase	338	53.5	11.6	307	2	H7292	conserved hypothet
266	54.5	11.8	445	1	S54140	D-serine permease	339	53.5	11.6	339	2	H71265	hypothetical prote
267	54.5	11.8	458	1	YTBSTR	tetracycline resis	340	53.5	11.6	346	2	D70558	probable cydB prot
268	54.5	11.8	458	1	YTSOG	tetracycline resis	341	53.5	11.6	357	2	F81679	chorismate synthas
269	54.5	11.8	458	1	YTB5U6	tetracycline resis	342	53.5	11.6	376	2	AF1943	multidrug-efflux t
270	54.5	11.8	458	2	JQ1211	tetracycline resis	343	53.5	11.6	378	2	T34372	hypothetical prote
271	54.5	11.8	458	2	S23743	tetracycline resis	344	53.5	11.6	383	2	T48018	hypothetical prote
272	54.5	11.8	483	1	A53595	tetracycline resis	345	53.5	11.6	410	2	A48585	transcription fact
273	54.5	11.8	484	2	T00158	allantoinase (EC 3	346	53.5	11.6	412	2	AH3274	macrolide-efflux p
274	54.5	11.8	501	2	E87239	amidase (EC 3.5.-	347	53.5	11.6	461	2	T06936	photosystem II chl
275	54.5	11.8	576	2	A49933	aldehyde dehydroge	348	53.5	11.6	495	2	I57680	potassium channel
276	54.5	11.8	586	2	T48672	proteinase SM tran	349	53.5	11.6	495	2	A40090	potassium channel
277	54.5	11.8	622	2	AC1236	ABC-type transport	350	53.5	11.6	495	2	B91113	potassium channel
278	54.5	11.8	622	2	T01467	acylttransferase (t	351	53.5	11.6	529	2	H84049	hypothetical prote
279	54.5	11.8	722	2	B71728	hypothetical prote	352	53.5	11.6	539	2	T32693	hypothetical prote
280	54.5	11.8	735	2	B69139	probable peptidase	353	53.5	11.6	546	2	S47300	gene F protein - r
281	54.5	11.8	735	2	E54343	hypothetical prote	354	53.5	11.6	553	1	VGNZMV	cell fusion glycop
282	54.5	11.8	895	2	S20582	dystroglycan - hum	355	53.5	11.6	556	2	T03114	tegument protein -
283	54.5	11.8	895	2	G87431	dystrophin-associ	356	53.5	11.6	571	1	H65169	probable transport
284	54.5	11.8	1044	2	T31072	pyruvate phosphate	357	53.5	11.6	571	2	D91206	probable cotranspo
285	54.5	11.8	1044	2	AB2158	heterocyst differe	358	53.5	11.6	571	2	F86052	probable cotranspo
286	54.5	11.8	1099	2	T14850	S-layer protein pr	359	53.5	11.6	594	2	T43246	amino acid transpo
287	54.5	11.8	1146	2	B35962	protein-tyrosine k	360	53.5	11.6	597	2	AH2351	serine/threonine k
288	54.5	11.8	1182	2	A35962	protein-tyrosine k	361	53.5	11.6	890	2	T35237	probable secreted
289	54	11.7	98	2	T17183	NADH2 dehydrogenas	362	53.5	11.6	945	2	S30398	aminopeptidase N h
290	54	11.7	98	2	T17348	NADH2 dehydrogenas	363	53.5	11.6	985	2	T10339	DNA-directed DNA p
291	54	11.7	154	1	MMBEI6	16.9K membrane pro	364	53.5	11.6	1045	2	E90705	hypothetical prote
292	54	11.7	168	2	S47881	NADH2 dehydrogenas	365	53.5	11.6	1045	2	H85555	hypothetical prote
293	54	11.7	188	2	A75382	hypothetical prote	366	53.5	11.6	1047	2	E64790	YbdE protein - Esc
294	54	11.7	248	1	PRMSC2	conserved hypothet	367	53.5	11.6	1075	2	S76433	cation efflux syst
295	54	11.7	259	2	C64481	hypothetical prote	368	53.5	11.6	1175	2	S51005	protein-tyrosine-p
296	54	11.7	292	2	F91044	transaldolase A [i	369	53.5	11.6	2037	2	T16881	hypothetical prote
297	54	11.7	316	2	A85889	transaldolase A [i	370	53.5	11.6	3566	1	A40701	tenascin-X precurs
298	54	11.7	316	2	G65021	transaldolase (EC	371	53	11.5	90	2	T33692	hypothetical prote
299	54	11.7	316	2	G65021	transaldolase (EC	372	53	11.5	148	2	A84636	similar to avrRpt2
300	54	11.7	328	2	A69218	hypothetical prote	373	53	11.5	154	1	F70002	conserved hypothet
301	54	11.7	346	2	C86413	cysteine proteinas	374	53	11.5	166	2	D58889	NADH2 dehydrogenas
302	54	11.7	351	2	I68620	rod outer segment	375	53	11.5	201	2	A71124	hypothetical prote
303	54	11.7	356	2	S66348	cysteine proteinas	376	53	11.5	202	2	JC6205	cell surface antig
304	54	11.7	356	2	B97742	hypothetical prote	377	53	11.5	210	2	UC5448	serine proteinase
305	54	11.7	359	2	F69061	hypothetical prote	378	53	11.5	214	2	AH0265	probable membrane
306	54	11.7	386	2	A72313	hypothetical prote	379	53	11.5	214	2	JC7930	small neutral amin
307	54	11.7	394	2	C64185	cell division prot	380	53	11.5	224	2	S67949	beta-tubulin ASL1
308	54	11.7	428	2	S08084	gene IV protein -	381	53	11.5	224	2	S73823	MG243 homolog H91
309	54	11.7	440	2	E84118	UDP-N-acetylglucos	382	53	11.5	257	2	D71544	hypothetical prote
310	54	11.7	456	2	AH0551	proline-specific p	383	53	11.5	264	2	A75076	membrane protein P
311	54	11.7	476	2	T40086	hypothetical prote	384	53	11.5	279	2	A95933	probable inositol
312	54	11.7	549	2	C86692	peptide-binding pr	385	53	11.5	300	2	B83100	inhibitor of chrom
313	54	11.7	558	2	AE1236	glycerol 3 phosph	386	53	11.5	306	2	A88040	protein F47F6.1 [i
314	54	11.7	573	1	S33212	INDA1 protein - fu	387	53	11.5	310	2	D87704	integral membrane
315	54	11.7	604	2	B84221	hypothetical prote	388	53	11.5	339	2	AG0165	L-allo-threonine a
316	54	11.7	625	2	T25373	hypothetical prote	389	53	11.5	342	2	A44965	cysteine proteinas
317	54	11.7	634	2	T33528	hypothetical prote	390	53	11.5	342	2	A45524	cysteine proteinas
318	54	11.7	787	2	T38224	probable glycosyl	391	53	11.5	364	2	AH1857	anthranilate phosph
319	54	11.7	869	2	A96558	probable protein k	392	53	11.5	376	2	E95879	probable sugar ABC
320	54	11.7	880	2	S49627	regulatory protein	393	53	11.5	377	2	A53044	geranylgeranyl-dip
321	54	11.7	885	2	G83260	aminopeptidase N p	394	53	11.5	385	2	A91178	probable membrane

103	58	12.6	185	2	AG1054	probable exported	176	56	12.1	594	2	A83096	probable permease
104	58	12.6	196	2	E75612	hypothetical prote	177	56	12.1	626	2	D70178	PTS system, fructo
105	58	12.6	215	2	AF0650	probable membrane	178	56	12.1	736	2	C69451	cationic amino aci
106	58	12.6	257	2	A64459	diphthine synthase	179	56	12.1	1118	2	C95385	probable adenylate
107	58	12.6	277	2	S44252	raffinose operon r	180	56	12.1	1305	2	AB0168	probable cell divi
108	58	12.6	368	2	T26425	hypothetical prote	181	56	12.1	2055	2	T30259	multiple PDZ domai
109	58	12.6	376	2	AH1795	hypothetical membr	182	56	12.1	3329	2	T42205	breast cancer susc
110	58	12.6	398	2	A82081	cell division prot	183	56	12.1	5170	2	T15348	hypothetical prote
111	58	12.6	462	2	F75588	probable kynurenin	184	55.5	12.0	245	2	A90527	hypothetical prote
112	58	12.6	4836	2	T14346	herc2 protein - mo	185	55.5	12.0	249	4	T44821	bacteriorhodopsin
113	57.5	12.5	71	2	D23876	vitellogenin B2 pr	186	55.5	12.0	254	2	F75496	conserved hypoteth
114	57.5	12.5	139	2	AF0685	hypothetical prote	187	55.5	12.0	256	2	E75401	hypothetical prote
115	57.5	12.5	324	2	T36805	conserved hypoteth	188	55.5	12.0	259	4	T44820	bacteriorhodopsin
116	57.5	12.5	342	2	A47673	photosystem II chl	189	55.5	12.0	262	1	RAHSB	bacteriorhodopsin
117	57.5	12.5	356	2	C72475	hypothetical prote	190	55.5	12.0	262	2	H84300	bacteriorhodopsin
118	57.5	12.5	374	2	T10415	virus envelope pro	191	55.5	12.0	270	2	B29934	pancreatic elastas
119	57.5	12.5	376	2	B83601	probable transport	192	55.5	12.0	299	2	B83243	hypothetical prote
120	57.5	12.5	461	2	AF0579	C4-dicarboxylate a	193	55.5	12.0	309	2	C95138	tagatose-6-phospha
121	57.5	12.5	523	2	B83629	probable ATP-bind	194	55.5	12.0	309	2	A98006	tagatose-6-phospha
122	57.5	12.5	528	2	I84205	potassium channel	195	55.5	12.0	316	2	G75388	hypothetical prote
123	57.5	12.5	594	2	B90586	transport protein	196	55.5	12.0	317	2	S16299	exoz protein - Rhi
124	57.5	12.5	636	2	S47299	gene F protein - r	197	55.5	12.0	317	2	B95975	acetyltransferase
125	57.5	12.5	662	2	T44219	hypothetical prote	198	55.5	12.0	344	2	S42648	photosystem II chl
126	57.5	12.5	662	2	T44034	hypothetical prote	199	55.5	12.0	344	2	AB2306	photosystem II chl
127	57.5	12.5	1902	1	B84658	lactocepin (EC 3.4	200	55.5	12.0	346	2	C71042	probable threonine
128	57	12.4	148	2	C84690	probable membrane	201	55.5	12.0	376	2	F72868	occlusion-derived
129	57	12.4	185	2	JN0766	adrenomedullin pre	202	55.5	12.0	383	2	S53379	probable membrane
130	57	12.4	258	2	F71251	probable uridine p	203	55.5	12.0	385	2	F86464	hypothetical prote
131	57	12.4	269	2	AG2268	hypothetical prote	204	55.5	12.0	389	2	B81347	probable aspartate
132	57	12.4	342	2	A30189	iron stress-induce	205	55.5	12.0	456	2	T22347	hypothetical prote
133	57	12.4	374	2	T05660	hypothetical prote	206	55.5	12.0	459	2	D86669	amino acid permeas
134	57	12.4	374	2	T00561	nodulin-like prote	207	55.5	12.0	545	2	A12327	hypothetical prote
135	57	12.4	385	2	T04725	hypothetical prote	208	55.5	12.0	609	2	S28283	hypothetical prote
136	57	12.4	440	2	H86312	F2H15.2 protein -	209	55.5	12.0	625	2	S13919	potassium channel
137	57	12.4	456	2	H69602	membrane protein,	210	55.5	12.0	648	2	C71658	probable pinosoma
138	57	12.4	457	2	B64769	proline transport	211	55.5	12.0	716	2	T03695	delta 1 pyroline-
139	57	12.4	457	2	D90685	proline permease t	212	55.5	12.0	851	2	T12503	hypothetical prote
140	57	12.4	457	2	H85535	proline permease t	213	55.5	12.0	946	1	A29550	methylenetetrahydr
141	57	12.4	461	2	D90711	C4-dicarboxylate a	214	55.5	12.0	1217	2	T22672	hypothetical prote
142	57	12.4	461	2	G4796	dcuC protein - Esc	215	55.5	12.0	1423	2	A49206	exo-beta-D-fructos
143	57	12.4	461	2	H85561	transport of dicar	216	55.5	12.0	2054	2	T46612	multi PDZ domain p
144	57	12.4	487	2	S73277	photosystem II 44K	217	55	11.9	52	2	T32956	hypothetical prote
145	56.5	12.3	114	2	E43559	homeotic protein R	218	55	11.9	52	2	T33694	hypothetical prote
146	56.5	12.3	187	2	S70186	21K protein - Shig	219	55	11.9	128	2	F71371	hypothetical prote
147	56.5	12.3	191	2	AD0905	probable exported	220	55	11.9	169	2	S18653	hypothetical prote
148	56.5	12.3	233	2	F70668	probable lipoprote	221	55	11.9	212	2	B82125	conserved hypoteth
149	56.5	12.3	258	2	D84336	uridine phosphoryl	222	55	11.9	268	2	S05471	embryonic abundan
150	56.5	12.3	361	2	S19552	potassium channel	223	55	11.9	268	2	S14068	seed protein precu
151	56.5	12.3	419	2	S22136	endothiapepsin (EC	224	55	11.9	288	2	T12462	hypothetical prote
152	56.5	12.3	471	2	T04911	hypothetical prote	225	55	11.9	312	2	B75405	endopeptidase-rela
153	56.5	12.3	485	2	E97506	potassium uptake p	226	55	11.9	334	2	S54438	hemin permease [va
154	56.5	12.3	500	2	F97025	spoVB related memb	227	55	11.9	336	2	AH0201	probable Zinc-bind
155	56.5	12.3	614	2	A69845	Na+/H+ antiporter	228	55	11.9	340	2	AF2896	hypothetical prote
156	56.5	12.3	670	1	E70040	conserved hypoteth	229	55	11.9	340	2	H97671	hypothetical prote
157	56.5	12.3	686	1	VGBENA	glycoprotein H pre	230	55	11.9	344	2	E84043	glycerolaldehyde-3-p
158	56.5	12.3	686	1	VGBEPK	glycoprotein H pre	231	55	11.9	357	2	A23641	RP2 protein, tesco
159	56.5	12.3	686	2	S15478	glycoprotein H - s	232	55	11.9	376	1	S17246	chorismate synthas
160	56.5	12.3	852	2	S25359	hypothetical prote	233	55	11.9	404	2	S34031	Ktr3 protein - yea
161	56	12.1	79	1	T1EPVK	K+ channel blocker	234	55	11.9	410	2	AH2895	hypothetical prote
162	56	12.1	196	2	F64231	hypothetical prote	235	55	11.9	410	2	C97671	probable maltose-b
163	56	12.1	222	2	F82353	conserved hypoteth	236	55	11.9	443	2	B86180	protein TIG11.3 [i
164	56	12.1	261	2	AB2966	conserved hypoteth	237	55	11.9	459	2	A87201	conserved hypoteth
165	56	12.1	261	2	B98317	ATP synthase chain	238	55	11.9	461	2	S57713	probable mannosyl
166	56	12.1	388	2	T09885	hypothetical prote	239	55	11.9	473	1	F2KK4C	photosystem II chl
167	56	12.1	411	2	B87586	metal ion efflux m	240	55	11.9	482	2	AG1147	P60 extracellular
168	56	12.1	436	2	G70058	hypothetical prote	241	55	11.9	484	2	A41487	protein P60 precu
169	56	12.1	440	2	C97376	probable transport	242	55	11.9	654	2	A96235	hydroxamate-depend
170	56	12.1	440	2	A12593	MFS permease limpo	243	55	11.9	654	2	AC3051	hypothetical prote
171	56	12.1	449	2	H70546	hypothetical prote	244	55	11.9	716	2	E69672	penicillin-binding
172	56	12.1	503	2	S36514	Li protein - human	245	55	11.9	2531	2	S18188	notch-1 protein homo
173	56	12.1	547	2	D95337	probable manganese	246	55	11.9	2531	2	A46019	translocon-associa
174	56	12.1	558	2	S29125	dimethylaniline mo	247	54.5	11.8	173	2	S33295	hypothetical prote
175	56	12.1	578	2	B37852	phosphotransferase	248	54.5	11.8	177	2	G75285	hypothetical prote

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 21, 2006, 19:45:28 ; Search time 41 Seconds
(without alignments)
208.861 Million cell updates/sec

Title: US-10-063-557-50
Perfect score: 461
Sequence: 1 MERVIALLLAGLTALEN.....HSPVPEKAIPITPGSATTC 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR 80:*

1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	256.5	55.6	87	2 I59391	transmembrane prot
2	241.5	52.4	88	2 S61552	mammary tumor prot
3	214.5	46.5	87	2 A55571	chloride conductan
4	126.5	27.4	92	2 A40533	CAMP-dependent pro
5	96.5	20.9	58	2 D46435	Na+/K+-exchanging
6	94.5	20.5	53	2 A46435	Na+/K+-exchanging
7	75.5	16.4	58	2 B46435	Na+/K+-exchanging
8	73.5	15.9	58	2 C46435	Na+/K+-exchanging
9	72	15.6	160	1 A61088	plastoquinol-plast
10	71	15.4	529	2 F69989	conserved hypothet
11	69	15.0	150	2 A80371	probable membrane
12	67.5	14.6	135	2 A05009	hypothetical prote
13	66.5	14.4	359	2 B86620	chorismate synthas
14	66.5	14.4	359	2 A72004	chorismate synthas
15	66.5	14.4	523	2 A38101	potassium channel
16	66	14.3	446	2 B90463	proline/betaine tr
17	64	13.9	525	2 A43531	potassium channel
18	63.5	13.8	309	2 AC1697	probable transport
19	63.5	13.8	309	2 A11325	probable transport
20	63.5	13.8	511	2 A46020	potassium channel
21	63.5	13.8	511	2 S07095	potassium channel
22	63.5	13.8	585	2 A39395	delayed rectifier
23	63.5	13.8	620	2 A70525	hypothetical prote
24	63	13.7	468	2 C96818	hypothetical prote
25	62.5	13.6	299	2 A38111	transcription regu
26	62.5	13.6	679	2 A42073	potassium channel
27	62.5	13.6	769	2 I56546	Shaw type potassi
28	62.5	13.6	910	2 F81974	leucine-tRNA ligas
29	62	13.4	381	2 AB2907	GGDEF family prote

30	62	13.4	393	2 B97682	ggdef family prote
31	62	13.4	589	2 U43295	uracil transport p
32	62	13.4	777	2 S30271	pyocin AP41 large
33	61.5	13.3	342	2 S75086	iron-stress chloro
34	61.5	13.3	433	2 B72025	flagellum-specific
35	61.5	13.3	433	2 A81513	virulence Atfase,
36	61.5	13.3	433	2 H86597	flagellum-specific
37	61.5	13.3	445	2 AD0962	DsdX permease [imp
38	61.5	13.3	990	2 JC8058	laeverin - human
39	61.5	13.3	1499	2 AC2555	hypothetical prote
40	61	13.2	268	2 C87295	conserved hypothet
41	61	13.2	355	2 I51157	major histocompati
42	61	13.2	461	2 B90984	O antigen flippase
43	61	13.2	463	2 A75151	damage-inducible p
44	61	13.2	463	2 E85829	O antigen flippase
45	61	13.2	463	2 G71191	probable DNA damag
46	61	13.2	520	2 D84471	probable membrane
47	60.5	13.1	295	2 C84830	probable protein k
48	60.5	13.1	312	2 B83749	sugar transport sy
49	60.5	13.1	326	2 C90272	hypothetical prote
50	60.5	13.1	354	2 E86276	hypothetical prote
51	60.5	13.1	427	2 E87669	conserved hypothet
52	60.5	13.1	463	2 A10388	probable proline-s
53	60.5	13.1	516	2 T47509	potassium channel
54	60.5	13.1	581	2 S17150	potassium channel
55	60.5	13.1	613	2 A39402	potassium channel
56	60.5	13.1	624	2 S22703	voltage-gated pota
57	60.5	13.1	728	2 B81370	phosphoribosylform
58	60	13.0	71	2 C23876	vitellogenin B1 pr
59	60	13.0	208	2 S36155	paired box protein
60	60	13.0	269	2 AH1970	type 4 prelin pe
61	60	13.0	342	2 S57652	transcription fact
62	60	13.0	412	2 A83461	hypothetical prote
63	60	13.0	497	1 WBEELM	membrane protein L
64	60	13.0	538	2 A65175	hypothetical 60.6
65	60	13.0	5232	2 A45086	HC-toxin synthetas
66	59.5	12.9	267	2 G86782	phosphomethylpyrim
67	59.5	12.9	298	2 A82387	amino acid ABC tra
68	59.5	12.9	356	2 T30361	occlusion-derived
69	59.5	12.9	527	2 A48076	glucose transporte
70	59.5	12.9	527	2 A45611	probable hexose tr
71	59	12.8	130	2 B85808	unknown protein en
72	59	12.8	175	2 T11087	NADH2 dehydrogenas
73	59	12.8	177	2 AH1669	probable NAD(p)H o
74	59	12.8	215	2 E85704	probable channel p
75	59	12.8	215	2 F90846	probable channel p
76	59	12.8	215	2 E64871	probable membrane
77	59	12.8	310	2 G87624	integral membrane
78	59	12.8	326	2 AB3607	3-oxoacyl-[acyl-ca
79	59	12.8	419	2 E90446	permease (imported
80	59	12.8	420	2 G96002	probable sugar upt
81	59	12.8	479	2 C95366	NADH2 dehydrogenas
82	59	12.8	558	2 A39322	glycerol 3 phospho
83	59	12.8	653	2 AB1599	potassium channel
84	59	12.8	654	2 S11049	potassium channel
85	59	12.8	660	2 S24125	potassium channel
86	59	12.8	802	2 JH0595	potassium channel
87	59	12.8	853	1 CHK1D1	potassium channel
88	59	12.8	857	2 I56529	potassium channel
89	59	12.8	858	2 S31761	potassium channel
90	58.5	12.7	182	2 C83600	hypothetical prote
91	58.5	12.7	384	2 A12962	cellulose synthesi
92	58.5	12.7	389	2 E98320	hypothetical prote
93	58.5	12.7	411	2 H75376	hypothetical prote
94	58.5	12.7	425	2 T50355	hypothetical prote
95	58.5	12.7	463	2 D87201	conserved hypothet
96	58.5	12.7	633	2 E86271	protein F16A14.4 [
97	58.5	12.7	876	2 G81029	leucine-tRNA ligas
98	58.5	12.7	1095	2 E96744	probable oligopept
99	58.5	12.7	1189	2 I39711	celE protein - Agr
100	58.5	12.7	2712	2 T30949	hypothetical prote
101	58.5	12.7	3864	2 D87757	protein C44E4.1a [
102	58	12.6	114	2 F69782	hypothetical prote

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Job time : 57 secs

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1430	48.5	10.5	1035	6	US-10-449-902-55142	Sequence 55142, A
1431	48.5	10.5	1035	7	US-11-056-355B-86863	Sequence 86863, A
1432	48.5	10.5	1036	6	US-10-539-228-160	Sequence 160, App
1433	48.5	10.5	1036	6	US-10-539-228-157	Sequence 157, App
1434	48.5	10.5	1052	6	US-10-449-902-46489	Sequence 46489, A
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1436	48.5	10.5	1382	7	US-11-174-307B-828	Sequence 828, App
1437	48.5	10.5	1382	7	US-11-174-307B-2402	Sequence 2402, Ap
1438	48.5	10.5	1399	7	US-11-330-403-2494	Sequence 2494, Ap
1439	48.5	10.5	1460	7	US-11-247-437-14	Sequence 14, Appl
1440	48.5	10.5	2303	7	US-11-335-891-31	Sequence 31, Appl
1441	48.5	10.4	21	7	US-11-311-454-72	Sequence 72, Appl
1442	48	10.4	73	7	US-11-366-486-914	Sequence 914, App
1443	48	10.4	75	6	US-10-449-902-44364	Sequence 44364, A
1444	48	10.4	95	6	US-10-449-902-37384	Sequence 37384, A
1445	48	10.4	114	6	US-10-612-783-5479	Sequence 5479, Ap
1446	48	10.4	120	7	US-11-361-977A-87	Sequence 87, Appl
1447	48	10.4	153	6	US-10-449-902-46328	Sequence 46328, A
1448	48	10.4	165	6	US-10-560-414-50	Sequence 50, Appl
1449	48	10.4	165	6	US-10-560-224-50	Sequence 50, Appl
1450	48	10.4	167	7	US-11-366-965-393	Sequence 393, App
1451	48	10.4	192	7	US-11-056-355B-82136	Sequence 82136, A
1452	48	10.4	191	7	US-11-056-355B-82135	Sequence 82135, A
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1457	48	10.4	246	6	US-10-805-394-4213	Sequence 4213, Ap
1458	48	10.4	254	7	US-11-266-747-460	Sequence 460, App
1459	48	10.4	259	6	US-10-449-902-30235	Sequence 30235, A
1460	48	10.4	259	6	US-10-449-902-30690	Sequence 30690, A
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1462	48	10.4	259	6	US-10-449-902-30767	Sequence 30767, A
1463	48	10.4	259	6	US-10-449-902-31699	Sequence 31699, A
1464	48	10.4	259	6	US-10-449-902-32099	Sequence 32099, A
1465	48	10.4	259	6	US-10-449-902-32375	Sequence 32375, A
1466	48	10.4	259	6	US-10-449-902-32541	Sequence 32541, A
1467	48	10.4	259	6	US-10-449-902-40510	Sequence 40510, A
1468	48	10.4	259	6	US-11-330-403-15182	Sequence 15182, A
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1475	48	10.4	327	6	US-11-056-355B-55556	Sequence 55556, A
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1477	48	10.4	329	7	US-11-293-697-3731	Sequence 3731, Ap
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1481	48	10.4	335	7	US-11-056-355B-117686	Sequence 117686, A
1482	48	10.4	335	7	US-11-330-403-17185	Sequence 17185, A
1483	48	10.4	341	7	US-10-449-902-33404	Sequence 33404, A
1484	48	10.4	346	7	US-11-056-355B-68846	Sequence 68846, A
1485	48	10.4	349	7	US-11-293-697-2684	Sequence 2684, Ap
1486	48	10.4	350	7	US-11-330-403-17232	Sequence 17232, A
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1488	48	10.4	360	6	US-10-449-902-47214	Sequence 47214, A
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1490	48	10.4	362	6	US-10-511-937-2509	Sequence 2509, Ap
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1493	48	10.4	382	7	US-11-434-137-182	Sequence 182, App
1494	48	10.4	382	7	US-11-434-184-182	Sequence 182, App
1495	48	10.4	382	7	US-11-434-199-182	Sequence 182, App
1496	48	10.4	382	7	US-11-434-203-182	Sequence 182, App
1497	48	10.4	392	6	US-10-449-902-42715	Sequence 42715, A
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1283	48.5	10.5	220	7	US-11-056-355B-9560	Sequence 9560, Ap	1356	48.5	10.5	423	7	US-11-434-184-3350	Sequence 3350, Ap
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1286	48.5	10.5	224	7	US-11-293-697-3499	Sequence 3499, Ap	1359	48.5	10.5	425	6	US-10-953-349-24528	Sequence 24528, A
1287	48.5	10.5	229	6	US-10-526-324-1638	Sequence 1638, Ap	1360	48.5	10.5	433	6	US-10-449-902-50765	Sequence 50765, A
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1290	48.5	10.5	233	7	US-11-056-355B-70825	Sequence 70825, A	1363	48.5	10.5	442	7	US-11-254-173-56	Sequence 56, Appl
1291	48.5	10.5	234	6	US-10-953-349-34000	Sequence 34000, A	1364	48.5	10.5	442	7	US-11-264-784-9	Sequence 9, Appl
1292	48.5	10.5	234	6	US-10-612-783-5624	Sequence 5624, Ap	1365	48.5	10.5	442	7	US-11-264-737-9	Sequence 9, Appl
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1301	48.5	10.5	257	7	US-11-056-355B-32029	Sequence 32029, A	1374	48.5	10.5	479	6	US-10-449-902-41636	Sequence 41636, A
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1316	48.5	10.5	284	7	US-11-090-997-1382	Sequence 1382, Ap	1389	48.5	10.5	527	6	US-10-449-902-44839	Sequence 44839, A
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1322	48.5	10.5	297	7	US-11-056-355B-111185	Sequence 111185, A	1395	48.5	10.5	560	7	US-11-056-355B-96003	Sequence 96003, A
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1325	48.5	10.5	312	7	US-11-330-403-8959	Sequence 8959, Ap	1398	48.5	10.5	577	6	US-10-449-902-52690	Sequence 52690, A
1326	48.5	10.5	321	6	US-10-449-902-44406	Sequence 44406, A	1399	48.5	10.5	584	6	US-10-522-758-41	Sequence 41, Appl
1327	48.5	10.5	333	6	US-10-953-349-24530	Sequence 24530, A	1400	48.5	10.5	590	7	US-11-056-355B-84411	Sequence 84411, A
1328	48.5	10.5	334	7	US-11-434-137-3496	Sequence 3496, Ap	1401	48.5	10.5	599	7	US-11-033-687-1	Sequence 1, Appl
1329	48.5	10.5	334	7	US-11-434-137-8732	Sequence 8732, Ap	1402	48.5	10.5	611	7	US-11-289-102-385	Sequence 385, Appl
1330	48.5	10.5	334	7	US-11-434-184-3496	Sequence 3496, Ap	1403	48.5	10.5	611	7	US-11-330-403-6742	Sequence 6742, Ap
1331	48.5	10.5	334	7	US-11-434-184-8732	Sequence 8732, Ap	1404	48.5	10.5	622	7	US-11-056-355B-76772	Sequence 76772, A
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1334	48.5	10.5	334	7	US-11-434-203-3496	Sequence 3496, Ap	1407	48.5	10.5	659	6	US-10-449-902-38329	Sequence 38329, A
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1139	49	10.6	353	6	US-10-560-224-41	Sequence 41, Appl	1212	49	10.6	569	7	US-11-056-355B-19937	Sequence 19937, A
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1141	49	10.6	363	6	US-10-545-557-21	Sequence 21, Appl	1214	49	10.6	574	7	US-11-317-847A-158	Sequence 158, App
1142	49	10.6	363	7	US-11-056-355B-25012	Sequence 25012, A	1215	49	10.6	622	7	US-11-330-403-10627	Sequence 10627, A
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1145	49	10.6	369	6	US-10-953-349-1136	Sequence 1136, Ap	1218	49	10.6	646	7	US-11-330-403-12708	Sequence 12708, A
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1149	49	10.6	369	7	US-11-056-355B-112089	Sequence 112089, A	1222	49	10.6	914	6	US-10-700-439-180	Sequence 180, App
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1154	49	10.6	377	7	US-11-056-355B-34739	Sequence 34739, A	1227	49	10.6	1207	7	US-11-273-537-25	Sequence 25, Appl
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1156	49	10.6	386	7	US-11-293-697-3254	Sequence 3254, Ap	1229	49	10.6	1506	6	US-10-669-920-1142	Sequence 1142, Ap
1157	49	10.6	389	7	US-11-330-403-11368	Sequence 11368, A	1230	49	10.6	1506	6	US-10-669-920-1153	Sequence 1153, Ap
1158	49	10.6	396	7	US-11-330-403-3920	Sequence 3920, Ap	1231	49	10.6	1522	7	US-11-174-307B-1928	Sequence 1928, Ap
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1160	49	10.6	417	7	US-11-330-403-3162	Sequence 3162, Ap	1233	49	10.6	2608	6	US-10-669-920-1144	Sequence 1144, Ap
1161	49	10.6	420	7	US-11-330-403-1125	Sequence 1125, Ap	1234	49	10.6	2608	6	US-10-669-920-1155	Sequence 1155, Ap
1162	49	10.6	421	7	US-11-056-355B-50117	Sequence 50117, A	1235	49	10.6	2902	6	US-10-669-920-1150	Sequence 1150, Ap
1163	49	10.6	423	6	US-10-449-902-45075	Sequence 45075, A	1236	49	10.6	2902	6	US-10-669-920-1161	Sequence 1161, Ap
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1165	49	10.6	443	6	US-10-669-920-691	Sequence 691, App	1238	49	10.6	2904	6	US-10-669-920-1157	Sequence 1157, Ap
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993	50	10.8	1703	7	US-11-455-703-8	Sequence 8, Appl	1066	49.5	10.7	428	6	US-10-612-903-4764	Sequence 4764, Ap
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843	50.5	11.0	372	7	US-11-056-355B-64023	Sequence 64023, A	916	50.5	11.0	1018	7	US-11-056-355B-73837	Sequence 73837, A
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852	50.5	11.0	414	7	US-11-434-137-3156	Sequence 3156, Ap	927	50	10.8	194	6	US-11-056-355B-53319	Sequence 53319, A
853	50.5	11.0	414	7	US-11-434-184-3156	Sequence 3156, Ap	928	50	10.8	194	6	US-10-953-349-17081	Sequence 17081, A
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860	50.5	11.0	469	6	US-10-540-898-292	Sequence 292, App	935	App	10.8	244	7	US-11-056-355B-53318	Sequence 53318, A
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863	50.5	11.0	476	6	US-10-449-902-35067	Sequence 35067, A	938	50	10.8	267	7	US-11-434-184-18	Sequence 18, Appl
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877	50.5	11.0	549	6	US-10-953-349-38451	Sequence 38451, A	952	50	10.8	375	6	US-10-953-349-12680	Sequence 12680, A
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891	50.5	11.0	654	7	US-11-434-184-6032	Sequence 6032, Ap	966	50	10.8	457	6	US-10-700-439-1502	Sequence 1502, App
892	50.5	11.0	654	7	US-11-434-199-6032	Sequence 6032, Ap	967	50	10.8	489	7	US-11-056-355B-5677	Sequence 5677, Ap
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912	50.5	11.0	990	7	US-11-056-355B-73839	Sequence 73839, A	987	50	10.8	949	7	US-11-056-355B-83268	Sequence 83268, A
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705	51	11.1	252	6	US-10-449-902-32186	Sequence 32186, A	778	51	11.1	666	6	US-10-953-349-11716	Sequence 11716, A
706	51	11.1	252	6	US-10-449-902-32302	Sequence 32302, A	779	51	11.1	666	7	US-11-056-355B-20632	Sequence 20632, A
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727	51	11.1	290	7	US-11-056-355B-28033	Sequence 28033, A	800	51	11.1	847	7	US-11-434-199-3236	Sequence 3236, Ap
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737	51	11.1	317	7	US-11-056-355B-28032	Sequence 28032, A	810	51	11.1	967	6	US-10-700-439-143	Sequence 143, App
738	51	11.1	317	6	US-11-056-355B-31622	Sequence 31622, A	811	51	11.1	967	7	US-11-387-011-2	Sequence 2, Appl
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740	51	11.1	327	7	US-11-056-355B-56644	Sequence 56644, A	813	51	11.1	1479	7	US-11-090-997-1262	Sequence 1262, Ap
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745	51	11.1	379	7	US-11-330-403-11043	Sequence 11043, A	818	50.5	11.0	86	6	US-10-449-902-38839	Sequence 38839, A
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755	51	11.1	421	6	US-11-330-403-2284	Sequence 2284, Ap	828	50.5	11.0	295	6	US-10-449-902-48737	Sequence 48737, A
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757	51	11.1	468	7	US-11-330-403-11433	Sequence 11433, A	830	50.5	11.0	303	7	US-11-056-355B-113337	Sequence 113337, A
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762	51	11.1	536	6	US-10-805-394-6061	Sequence 6061, Ap	835	50.5	11.0	330	7	US-11-434-137-6080	Sequence 6080, Ap
763	51	11.1	546	7	US-11-056-355B-44093	Sequence 44093, A	836	50.5	11.0	330	7	US-11-434-184-6080	Sequence 6080, Ap
764	51	11.1	546	7	US-11-056-355B-73985	Sequence 73985, A	837	50.5	11.0	330	7	US-11-434-199-6080	Sequence 6080, Ap
765	51	11.1	549	6	US-11-330-403-1699	Sequence 1699, Ap	838	50.5	11.0	330	7	US-11-434-203-6080	Sequence 6080, Ap
766	51	11.1	549	6	US-10-449-902-51736	Sequence 51736, A	839	50.5	11.0	341	6	US-10-449-902-48890	Sequence 48890, A
767	51	11.1	551	7	US-11-330-403-7070	Sequence 7070, Ap	840	50.5	11.0	363	6	US-10-449-902-49601	Sequence 49601, A
768	51	11.1	560	7	US-11-330-403-5799	Sequence 5799, Ap	841	50.5	11.0	364	6	US-10-612-783-4769	Sequence 4769, Ap

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545	52.5	11.4	6011	7	US-11-330-623-8	Sequence 8, Appl	624	51.5	11.2	318	7	US-11-330-403-2061	Sequence 2061, Ap
546	52	11.3	85	6	US-10-449-902-33923	Sequence 33923, A	625	51.5	11.2	327	6	US-10-953-349-15347	Sequence 15347, A
547	52	11.3	162	6	US-10-449-902-41668	Sequence 41668, A	626	51.5	11.2	327	7	US-11-056-355B-55937	Sequence 55937, A
548	52	11.3	207	6	US-10-953-349-1449	Sequence 1449, Ap	627	51.5	11.2	337	6	US-10-805-394-6658	Sequence 6658, Ap
549	52	11.3	207	7	US-11-056-355B-35018	Sequence 35018, A	628	51.5	11.2	344	7	US-11-434-137-3460	Sequence 3460, Ap
550	52	11.3	207	7	US-11-056-355B-41975	Sequence 41975, A	629	51.5	11.2	344	7	US-11-434-184-3460	Sequence 3460, Ap
551	52	11.3	207	7	US-11-056-355B-74387	Sequence 74387, A	630	51.5	11.2	344	7	US-11-434-199-3460	Sequence 3460, Ap
552	52	11.3	211	7	US-11-441-587-18	Sequence 18, Appl	631	51.5	11.2	344	7	US-11-434-203-3460	Sequence 3460, Ap
553	52	11.3	215	6	US-10-953-349-29195	Sequence 29195, A	632	51.5	11.2	349	6	US-10-953-349-15346	Sequence 15346, A
554	52	11.3	215	7	US-11-056-355B-63742	Sequence 63742, A	633	51.5	11.2	349	7	US-11-056-355B-55936	Sequence 55936, A
555	52	11.3	226	7	US-11-051-725-175	Sequence 175, App	634	51.5	11.2	373	6	US-10-953-349-15345	Sequence 15345, A
556	52	11.3	250	6	US-10-449-902-51855	Sequence 51855, A	635	51.5	11.2	373	7	US-11-056-355B-55935	Sequence 55935, A
557	52	11.3	260	6	US-10-652-846-8	Sequence 8, Appl	636	51.5	11.2	377	7	US-11-357-204-9	Sequence 9, Appl
558	52	11.3	297	6	US-11-295-040-10	Sequence 10, Appl	637	51.5	11.2	378	6	US-10-669-920-490	Sequence 490, App
559	52	11.3	297	6	US-10-374-780A-2898	Sequence 2898, Ap	638	51.5	11.2	378	6	US-10-669-920-493	Sequence 493, App
560	52	11.3	304	7	US-11-051-725-142	Sequence 142, App	639	51.5	11.2	378	6	US-10-669-920-495	Sequence 495, App
561	52	11.3	324	7	US-11-051-725-159	Sequence 159, App	640	51.5	11.2	378	7	US-11-056-355B-57491	Sequence 57491, A
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572	52	11.3	360	6	US-11-056-355B-63741	Sequence 63741, A	651	51.5	11.2	474	7	US-11-090-997-300	Sequence 300, App
573	52	11.3	375	6	US-10-953-349-29193	Sequence 29193, A	652	51.5	11.2	474	7	US-11-361-871-24	Sequence 24, Appl
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578	52	11.3	437	6	US-10-953-349-21135	Sequence 21135, A	657	51.5	11.2	511	7	US-11-330-403-2770	Sequence 2770, Ap
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580	52	11.3	470	6	US-10-953-349-21134	Sequence 21134, A	659	51.5	11.2	537	6	US-10-486-306-13	Sequence 13, Appl
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582	52	11.3	488	6	US-10-612-783-6593	Sequence 6593, Ap	661	51.5	11.2	549	7	US-11-358-419-32	Sequence 32, Appl
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584	52	11.3	512	7	US-11-330-403-487	Sequence 487, App	663	51.5	11.2	556	6	US-10-449-902-31689	Sequence 31689, A
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586	52	11.3	581	7	US-11-330-403-916	Sequence 916, App	665	51.5	11.2	616	6	US-10-526-324-1280	Sequence 1280, Ap
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590	52	11.3	687	6	US-10-805-394-6127	Sequence 6127, Ap	669	51.5	11.2	645	6	US-10-539-228-364	Sequence 364, App
591	52	11.3	944	6	US-10-449-902-46707	Sequence 46707, A	670	51.5	11.2	653	7	US-11-090-997-1306	Sequence 1306, Ap
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594	52	11.3	2057	7	US-11-011-702-29	Sequence 29, Appl	673	51.5	11.2	889	6	US-10-449-902-55069	Sequence 55069, A
595	52	11.3	2057	7	US-11-011-702-30	Sequence 30, Appl	674	51.5	11.2	889	6	US-10-449-902-55493	Sequence 55493, A
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598	52	11.3	2138	6	US-10-343-503-124	Sequence 124, App	677	51.5	11.2	2301	7	US-11-335-891-30	Sequence 30, Appl
599	52	11.3	2169	7	US-11-051-725-5	Sequence 5, Appl	678	51.5	11.2	2303	7	US-11-335-891-32	Sequence 32, Appl
600	52	11.3	2192	7	US-11-051-725-8	Sequence 8, Appl	679	51	11.1	127	6	US-10-953-349-1262	Sequence 1262, A
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607	51.5	11.2	187	7	US-11-056-355B-27748	Sequence 27748, A	686	51	11.1	209	6	US-10-953-349-23225	Sequence 23225, A
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612	51.5	11.2	212	6	US-11-056-355B-27747	Sequence 27747, A	691	51	11.1	228	7	US-11-056-355B-103837	Sequence 103837, A
613	51.5	11.2	235	7	US-11-056-355B-31337	Sequence 31337, A	692	51	11.1	228	7	US-11-056-355B-115076	Sequence 115076, A
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615	51.5	11.2	245	7	US-11-056-355B-65232	Sequence 65232, A	694	51	11.1	234	7	US-11-056-355B-74802	Sequence 74802, A
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399	53.5	11.6	271	7	US-11-434-184-7984	Sequence 7984, Ap	472	53	11.5	637	6	US-10-953-349-7922	Sequence 7922, Ap
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405	53.5	11.6	347	6	US-10-612-783-4612	Sequence 4612, Ap	478	53	11.5	648	7	US-11-056-355B-84746	Sequence 84746, A
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411	53.5	11.6	383	7	US-11-330-403-18468	Sequence 18468, A	484	53	11.5	702	6	US-10-953-349-7921	Sequence 7921, Ap
412	53.5	11.6	384	6	US-10-526-324-1723	Sequence 1723, Ap	485	53	11.5	702	7	US-11-056-355B-39889	Sequence 39889, A
413	53.5	11.6	384	6	US-10-330-403-16471	Sequence 16471, A	486	53	11.5	752	7	US-11-056-355B-85707	Sequence 85707, A
414	53.5	11.6	403	7	US-11-265-762-46	Sequence 46, Appl	487	53	11.5	1070	6	US-10-524-910-1	Sequence 1, Appl
415	53.5	11.6	405	6	US-10-449-902-36521	Sequence 36521, A	488	53	11.5	1070	6	US-10-570-909-80	Sequence 80, Appl
416	53.5	11.6	405	6	US-10-449-902-54849	Sequence 54849, A	489	53	11.5	1070	6	US-10-570-909-80	Sequence 80, Appl
417	53.5	11.6	482	7	US-11-056-355B-73785	Sequence 73785, A	490	53	11.5	1070	7	US-11-365-989-214	Sequence 214, Ap
418	53.5	11.6	485	7	US-11-056-355B-86768	Sequence 86768, A	491	53	11.5	1146	6	US-10-620-061-9	Sequence 9, Appl
419	53.5	11.6	485	7	US-11-056-355B-86767	Sequence 86767, A	492	53	11.5	1324	6	US-10-833-833-40	Sequence 40, Appl
420	53.5	11.6	495	7	US-11-313-450-19	Sequence 19, Appl	493	53	11.5	1463	6	US-10-833-833-36	Sequence 36, Appl
421	53.5	11.6	504	7	US-11-056-355B-86767	Sequence 86767, A	494	53	11.5	1463	6	US-10-833-833-38	Sequence 38, Appl
422	53.5	11.6	514	7	US-11-056-355B-86766	Sequence 86766, A	495	52.5	11.4	159	6	US-10-953-349-9133	Sequence 9133, Ap
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430	53	11.5	219	6	US-10-805-394-5067	Sequence 5067, Ap	503	52.5	11.4	292	7	US-11-056-355B-9533	Sequence 9533, Ap
431	53	11.5	232	6	US-10-449-902-32304	Sequence 32304, A	504	52.5	11.4	292	7	US-11-056-355B-11156	Sequence 11156, A
432	53	11.5	237	6	US-11-319-952-66	Sequence 66, Appl	505	52.5	11.4	292	7	US-11-056-355B-11207	Sequence 11207, A
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436	53	11.5	256	7	US-11-330-403-2298	Sequence 2298, Ap	509	52.5	11.4	324	6	US-10-545-100-9	Sequence 9, Appl
437	53	11.5	260	6	US-10-449-902-52480	Sequence 52480, A	510	52.5	11.4	342	6	US-10-612-783-6487	Sequence 6487, Ap
438	53	11.5	305	6	US-10-652-846-75	Sequence 75, Appl	511	52.5	11.4	354	7	US-11-056-355B-9531	Sequence 9531, Ap
439	53	11.5	309	6	US-10-449-902-37486	Sequence 37486, A	512	52.5	11.4	354	7	US-11-056-355B-11154	Sequence 11154, A
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444	53	11.5	357	7	US-11-330-403-13715	Sequence 13715, A	517	52.5	11.4	369	6	US-10-805-394-5658	Sequence 5658, Ap
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446	53	11.5	357	7	US-11-056-355B-95046	Sequence 95046, A	519	52.5	11.4	374	6	US-10-449-902-32419	Sequence 32419, A
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449	53	11.5	362	7	US-11-056-355B-16023	Sequence 16023, A	522	52.5	11.4	458	6	US-10-449-902-56530	Sequence 56530, A
450	53	11.5	376	7	US-11-056-355B-16022	Sequence 16022, A	523	52.5	11.4	468	6	US-10-805-394-4777	Sequence 4777, Ap
451	53	11.5	394	7	US-11-056-355B-16021	Sequence 16021, A	524	52.5	11.4	502	7	US-11-056-355B-40742	Sequence 40742, Ap
452	53	11.5	399	7	US-11-056-355B-90865	Sequence 90865, A	525	52.5	11.4	502	7	US-11-056-355B-105201	Sequence 105201, A
453	53	11.5	399	7	US-11-056-355B-94621	Sequence 94621, A	526	52.5	11.4	502	7	US-11-056-355B-116440	Sequence 116440, A
454	53	11.5	421	7	US-11-330-403-15378	Sequence 15378, A	527	52.5	11.4	537	6	US-10-449-902-47135	Sequence 47135, A
455	53	11.5	421	7	US-11-330-403-11121	Sequence 11121, A	528	52.5	11.4	551	7	US-11-236-238-29	Sequence 29, Appl
456	53	11.5	442	7	US-11-056-355B-85709	Sequence 85709, A	529	52.5	11.4	583	6	US-10-449-902-43575	Sequence 43575, A
457	53	11.5	443	7	US-11-056-355B-79230	Sequence 79230, A	530	52.5	11.4	583	7	US-10-449-902-48162	Sequence 48162, A
458	53	11.5	469	7	US-11-330-403-9133	Sequence 9133, Ap	531	52.5	11.4	593	7	US-11-056-355B-40741	Sequence 40741, A
459	53	11.5	524	7	US-11-056-355B-78201	Sequence 78201, A	532	52.5	11.4	593	7	US-11-056-355B-105200	Sequence 105200, A
460	53	11.5	528	7	US-11-056-355B-80748	Sequence 80748, A	533	52.5	11.4	593	7	US-11-056-355B-116439	Sequence 116439, A
461	53	11.5	548	7	US-11-056-355B-70616	Sequence 70616, A	534	52.5	11.4	612	7	US-11-056-355B-40740	Sequence 40740, A
462	53	11.5	548	7	US-11-056-355B-80747	Sequence 80747, A	535	52.5	11.4	616	7	US-11-056-355B-105199	Sequence 105199, A
463	53	11.5	554	7	US-11-056-355B-90864	Sequence 90864, A	536	52.5	11.4	616	7	US-11-056-355B-116438	Sequence 116438, A
464	53	11.5	554	7	US-11-056-355B-94620	Sequence 94620, A	537	52.5	11.4	673	6	US-10-449-902-54937	Sequence 54937, A
465	53	11.5	577	6	US-10-953-349-7923	Sequence 7923, Ap	538	52.5	11.4	763	7	US-11-311-454-88	Sequence 88, Appl
466	53	11.5	577	7	US-11-056-355B-39891	Sequence 39891, A	539	52.5	11.4	800	6	US-10-449-902-34842	Sequence 34842, A
467	53	11.5	577	7	US-11-056-355B-70615	Sequence 70615, A	540	52.5	11.4	1000	6	US-10-743-891A-25	Sequence 25, Appl
468	53	11.5	577	7	US-11-056-355B-84485	Sequence 84485, A	541	52.5	11.4	1005	7	US-11-311-454-2	Sequence 2, Appl
469	53	11.5	603	7	US-11-056-355B-70555	Sequence 70555, A	542	52.5	11.4	1373	7	US-11-311-454-1	Sequence 1, Appl
470	53	11.5	607	7	US-11-056-355B-78200	Sequence 78200, A	543	52.5	11.4	2000	7	US-11-311-454-82	Sequence 82, Appl

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254	55	11.9	152	7	US-11-056-355B-113903	Sequence 113903, A	327	54	11.7	139	7	US-11-056-355B-15263	Sequence 15263, A
255	55	11.9	159	7	US-11-434-137-1062	Sequence 1062, Ap	328	54	11.7	194	7	US-11-056-355B-10517	Sequence 10517, A
256	55	11.9	159	7	US-11-434-184-1062	Sequence 1062, Ap	329	54	11.7	194	7	US-11-056-355B-11187	Sequence 11187, A
257	55	11.9	159	7	US-11-434-199-1062	Sequence 1062, Ap	330	54	11.7	237	7	US-11-056-355B-10516	Sequence 10516, A
258	55	11.9	159	7	US-11-434-203-1062	Sequence 1062, Ap	331	54	11.7	237	7	US-11-056-355B-11186	Sequence 11186, A
259	55	11.9	185	7	US-11-056-355B-38484	Sequence 38484, A	332	54	11.7	246	7	US-11-056-355B-15262	Sequence 15262, A
260	55	11.9	185	7	US-11-056-355B-38876	Sequence 38876, A	333	54	11.7	249	7	US-10-953-349-17130	Sequence 17130, A
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262	55	11.9	187	7	US-11-056-355B-61948	Sequence 61948, A	335	54	11.7	253	6	US-10-953-349-17129	Sequence 17129, A
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266	55	11.9	277	7	US-11-056-355B-38875	Sequence 38875, A	339	54	11.7	290	6	US-10-449-902-32176	Sequence 32176, A
267	55	11.9	287	6	US-10-449-902-33881	Sequence 33881, A	340	54	11.7	290	6	US-10-449-902-32492	Sequence 32492, A
268	55	11.9	306	6	US-10-953-349-23327	Sequence 23327, A	341	54	11.7	290	6	US-10-449-902-36887	Sequence 36887, A
269	55	11.9	306	6	US-11-056-355B-54406	Sequence 54406, A	342	54	11.7	290	6	US-10-449-902-37012	Sequence 37012, A
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273	55	11.9	410	6	US-10-953-349-23326	Sequence 23326, A	346	54	11.7	304	7	US-11-056-355B-83069	Sequence 83069, A
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281	55	11.9	2505	6	US-10-669-920-15	Sequence 15, Appl	354	54	11.7	340	7	US-11-056-355B-74240	Sequence 74240, A
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283	54.5	11.8	158	7	US-11-056-355B-115990	Sequence 115990, A	356	54	11.7	346	7	US-11-056-355B-83067	Sequence 83067, App
284	54.5	11.8	165	7	US-11-056-355B-104750	Sequence 104750, A	357	54	11.7	346	7	US-11-339-733-60	Sequence 60, Appl
285	54.5	11.8	165	7	US-11-056-355B-115989	Sequence 115989, A	358	54	11.7	355	6	US-10-953-349-31241	Sequence 31241, A
286	54.5	11.8	185	6	US-10-374-780A-106	Sequence 106, App	359	54	11.7	355	6	US-10-526-324-2125	Sequence 2125, Ap
287	54.5	11.8	185	7	US-11-056-355B-22151	Sequence 22151, A	360	54	11.7	357	7	US-11-056-355B-65700	Sequence 65700, A
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289	54.5	11.8	185	7	US-11-056-355B-115988	Sequence 115988, A	362	54	11.7	357	7	US-11-056-355B-84877	Sequence 84877, A
290	54.5	11.8	189	6	US-10-449-902-39228	Sequence 39228, A	363	54	11.7	360	7	US-11-056-355B-84876	Sequence 84876, A
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295	54.5	11.8	276	6	US-10-353-349-15535	Sequence 15535, A	368	54	11.7	404	7	US-11-330-403-17492	Sequence 17492, A
296	54.5	11.8	280	6	US-10-449-902-41443	Sequence 41443, A	369	54	11.7	404	7	US-11-366-486-939	Sequence 939, App
297	54.5	11.8	283	7	US-11-330-403-10306	Sequence 10306, A	370	54	11.7	451	7	US-11-056-355B-59741	Sequence 59741, A
298	54.5	11.8	293	6	US-10-953-349-38938	Sequence 38938, A	371	54	11.7	470	7	US-11-366-486-673	Sequence 673, App
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307	54.5	11.8	384	7	US-10-340-318-4	Sequence 4, Appl	380	53.5	11.6	149	7	US-11-056-355B-32323	Sequence 32323, A
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310	54.5	11.8	445	7	US-11-289-989-15	Sequence 15, Appl	383	53.5	11.6	159	7	US-11-056-355B-28732	Sequence 28732, A
311	54.5	11.8	478	6	US-10-449-902-47028	Sequence 47028, A	384	53.5	11.6	159	7	US-11-056-355B-32322	Sequence 32322, A
312	54.5	11.8	481	7	US-11-449-111-77	Sequence 77, Appl	385	53.5	11.6	162	7	US-11-330-403-3442	Sequence 3442, Ap
313	54.5	11.8	509	6	US-10-449-902-47261	Sequence 47261, A	386	53.5	11.6	162	7	US-11-056-355B-101050	Sequence 101050, A
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316	54.5	11.8	815	6	US-10-449-902-52285	Sequence 52285, A	389	53.5	11.6	215	7	US-11-056-355B-5083	Sequence 5083, Ap
317	54.5	11.8	859	6	US-10-449-902-43366	Sequence 43366, A	390	53.5	11.6	221	7	US-11-056-355B-5083	Sequence 369, App
318	54.5	11.8	1146	7	US-11-274-081-3	Sequence 3, Appl	391	53.5	11.6	221	7	US-11-330-403-369	Sequence 369, App
319	54.5	11.8	1146	7	US-11-191-644-4	Sequence 4, Appl	392	53.5	11.6	239	7	US-11-319-952-71	Sequence 71, Appl
320	54.5	11.8	1182	7	US-11-191-644-5	Sequence 5, Appl	393	53.5	11.6	244	6	US-10-544-944-6	Sequence 6, Appl
321	54.5	11.8	1251	6	US-10-449-902-49449	Sequence 49449, A	394	53.5	11.6	244	6	US-10-546-435-4	Sequence 11, Appl
322	54.5	11.8	1385	7	US-11-191-644-20	Sequence 20, Appl	395	53.5	11.6	244	6	US-10-652-846-11	Sequence 11, Appl
323	54.5	11.8	1406	7	US-11-191-644-18	Sequence 18, Appl	396	53.5	11.6	244	7	US-11-319-952-84	Sequence 84, Appl
324	54	11.7	55	7	US-11-366-486-742	Sequence 742, App	397	53.5	11.6	259	7	US-11-330-403-6661	Sequence 6661, Ap

106	58.5	12.7	320	7	US-11-056-355B-117774	Sequence 117774,	179	57	12.4	184	7	US-11-056-355B-103216	Sequence 103216,
107	58.5	12.7	321	7	US-11-056-355B-46714	Sequence 26714, A	180	57	12.4	184	7	US-11-056-355B-114455	Sequence 114455,
108	58.5	12.7	350	7	US-11-056-355B-36367	Sequence 36367, A	181	57	12.4	210	7	US-11-056-355B-35886	Sequence 35886, A
109	58.5	12.7	356	7	US-11-056-355B-36366	Sequence 36366, A	182	57	12.4	210	7	US-11-056-355B-74435	Sequence 74435, A
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112	58.5	12.7	377	7	US-11-056-355B-39929	Sequence 39929, A	185	57	12.4	233	7	US-11-056-355B-14552	Sequence 14552, A
113	58.5	12.7	377	7	US-11-056-355B-42537	Sequence 42537, A	186	57	12.4	240	7	US-11-056-355B-20732	Sequence 20732, A
114	58.5	12.7	377	7	US-11-056-355B-75575	Sequence 75575, A	187	57	12.4	242	7	US-11-056-355B-77238	Sequence 77238, A
115	58.5	12.7	377	7	US-11-056-355B-98547	Sequence 98547, A	188	57	12.4	242	6	US-10-953-349-7055	Sequence 7055, Ap
116	58.5	12.7	377	7	US-11-056-355B-109786	Sequence 109786,	189	57	12.4	253	7	US-11-056-355B-20731	Sequence 20731, A
117	58.5	12.7	383	7	US-11-058-746-6	Sequence 6, Appl	190	57	12.4	253	7	US-11-056-355B-37018	Sequence 37018, A
118	58.5	12.7	383	7	US-11-056-355B-28875	Sequence 28875, A	191	57	12.4	253	7	US-11-056-355B-74211	Sequence 74211, A
119	58.5	12.7	383	7	US-11-056-355B-32465	Sequence 32465, A	192	57	12.4	260	7	US-11-366-965-257	Sequence 257, App
120	58.5	12.7	383	7	US-11-056-355B-39928	Sequence 39928, A	193	57	12.4	309	7	US-11-056-355B-26769	Sequence 26769, A
121	58.5	12.7	383	7	US-11-056-355B-42536	Sequence 42536, A	194	57	12.4	340	6	US-10-449-902-40749	Sequence 40749, A
122	58.5	12.7	383	7	US-11-056-355B-75574	Sequence 75574, A	195	57	12.4	341	7	US-11-056-355B-26768	Sequence 26768, A
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124	58.5	12.7	383	7	US-11-056-355B-109785	Sequence 109785,	197	57	12.4	366	6	US-10-953-349-7054	Sequence 7054, Ap
125	58.5	12.7	385	6	US-10-449-902-39728	Sequence 39728, A	198	57	12.4	366	7	US-11-056-355B-37017	Sequence 37017, A
126	58.5	12.7	409	7	US-11-330-403-6443	Sequence 6443, Ap	199	57	12.4	366	7	US-11-056-355B-74210	Sequence 74210, A
127	58.5	12.7	557	7	US-11-056-355B-83002	Sequence 83002, A	200	57	12.4	374	7	US-11-056-355B-26767	Sequence 26767, A
128	58.5	12.7	567	7	US-11-056-355B-83001	Sequence 83001, A	201	57	12.4	374	7	US-11-056-355B-77237	Sequence 77237, A
129	58.5	12.7	577	7	US-11-174-307B-4440	Sequence 4440, Ap	202	57	12.4	384	6	US-10-449-902-36950	Sequence 36950, A
130	58.5	12.7	1095	7	US-11-056-355B-71583	Sequence 71583, A	203	57	12.4	384	6	US-10-449-902-38775	Sequence 38775, A
131	58.5	12.7	1118	7	US-11-056-355B-73209	Sequence 73209, A	204	57	12.4	385	6	US-10-953-349-7053	Sequence 7053, Ap
132	58	12.6	295	7	US-11-056-355B-9964	Sequence 9964, Ap	205	57	12.4	385	7	US-11-056-355B-20730	Sequence 20730, A
133	58	12.6	333	7	US-11-293-697-4461	Sequence 4461, Ap	206	57	12.4	385	7	US-11-056-355B-37016	Sequence 37016, A
134	58	12.6	352	7	US-11-056-355B-9963	Sequence 9963, Ap	207	57	12.4	385	7	US-11-056-355B-74209	Sequence 74209, A
135	58	12.6	352	7	US-11-056-355B-9962	Sequence 9962, Ap	208	56.5	12.3	352	7	US-11-056-355B-58174	Sequence 58174, A
136	58	12.6	356	6	US-10-612-783-5903	Sequence 5903, Ap	209	56.5	12.3	356	7	US-11-056-355B-58173	Sequence 58173, A
137	58	12.6	366	7	US-11-056-355B-96643	Sequence 96643, Ap	210	56.5	12.3	356	7	US-11-056-355B-58172	Sequence 58172, A
138	58	12.6	366	7	US-11-056-355B-73743	Sequence 73743, A	211	56.5	12.3	356	7	US-11-056-355B-58172	Sequence 58172, A
139	58	12.6	367	7	US-11-056-355B-96642	Sequence 96642, A	212	56.5	12.3	316	7	US-11-330-403-18366	Sequence 18366, A
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11	94	20.4	178	7 US-11-090-997-1144	Sequence 1144, Ap
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744	461	100.0	89	5	US-10-950-374-262
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1325	105.5	22.9	110	5	US-10-450-763-56705	Sequence 56705, App
1326	94	20.4	115	4	US-10-352-272-2	Sequence 2, Appl
1327	94	20.4	178	3	US-09-833-245-1532	Sequence 1532, App
1328	94	20.4	178	3	US-09-985-153-92	Sequence 92, Appl
1329	94	20.4	178	3	US-09-985-153-93	Sequence 93, Appl
1330	94	20.4	178	3	US-09-985-153-94	Sequence 94, Appl
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Search completed: November 21, 2006, 19:59:06

Job time : 213 secs

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REFERENCE/DOCKET NUMBER: PF-0141 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 951423
US-08-738-127-5

Query Match 55.6%; Score 256.5; DB 1; Length 87;
Best Local Similarity 61.5%; Pred. No. 3.6e-25;
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Db 1 MEGITCAFLIVLAGLPVLEANGP-VDKGSPYYDWESLQLGGMIFGGLLCIAGIAMALSG 59
Qy 60 KCKYKSSQKHSP--VPEKAIPLITPGSATT 88
Db 60 KCK---CRNHTPSLSPEKVTPLITPGSAST 87

Search completed: November 21, 2006, 19:46:23
Job time : 72 secs


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; APPLICATION NUMBER: US/08/725,531
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0128 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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Best Local Similarity 61.5%; Pred. No. 3.6e-25;
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DB 60 KCK---CRRHPTSSLPEKVTPLTIPGSAST 87

RESULT 15
US-08-738-127-5
; Sequence 5, Application US/08738127
; Patent No. 5919655
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.

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; PRIOR FILING DATE: 1998-07-09

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Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 262, Application US/09989293A
; Patent No. 7034136
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
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Query Match          100.0%; Score 461; DB 3; Length 89;
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Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MERVTLALLLGLTALANDPPANKDDPPYDWNKQLSGLICGGLAIAAGIAVLSGK 60

QY 61 CKYSSKQKHSVPPEKAIPITPGSATTC 89
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: KJavin, Ivar J.
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; APPLICANT: Pan, James
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC38
; CURRENT APPLICATION NUMBER: US/09/997,653
; CURRENT FILING DATE: 2001-11-15
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 461; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MERVTLALLLLAGLTALFANDPFANKDDPFYDWNKQLSLGICGGLLAIAAGIAAVLSK 60

Qy 61 CKYKSSQKHSPVPEKAIPLTIPGSATTC 89
Db 61 CKYKSSQKHSPVPEKAIPLTIPGSATTC 89

RESULT 10
US-09-997-349-362
; Sequence 262, Application US/09997349
; Patent No. 7034106
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC37
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 461; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 2,2e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CKYKSQKQHSVPVPEKAIPITPGSATTC 89
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RESULT 9
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; Sequence 262, Application US/09989728
; Patent No. 7029873
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C72
; CURRENT APPLICATION NUMBER: US/09/989,728
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 461; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2,2e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERVTLALLLAGLTALEANDPFANKDDPPYDWKNLQSLGICGGLAATAGIAAVLSGK 60
Db 1 MERVTLALLLAGLTALEANDPFANKDDPPYDWKNLQSLGICGGLAATAGIAAVLSGK 60

Qy 61 CKYKSSQKHSPVPEKAIPILITPGSATTC 89
Db 61 CKYKSSQKHSPVPEKAIPILITPGSATTC 89

RESULT 7
US-09-389-726-262
; Sequence 262, Application US/09389726
; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC60

; CURRENT APPLICATION NUMBER: US/09/989,726
; CURRENT FILING DATE: 2001-11-19
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;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P27301C61
;; CURRENT APPLICATION NUMBER: US/09/989,735
;; CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE:	1998-06-25

	Query Match	100.0%;	Score 461;	DB 2;	Length 89;
	Best Local Similarity	100.0%;	Pred. No. 2.2e-51;		
	Matches	89;	Mismatches	0;	Gaps 0;
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Dd	1	MERTVLALLLGLTALALEANDPFANKDDPFYDWKNQLSLGILCGLLIAGIAIVLSGK	60		
Qy	61	CKYKSSQKHSPVPEKAIPLIITPGSATTCC	89		
Dd	61	CKYKSSQKHSPVPEKAIPLIITPGSATTCC	89		

RESULT 6
US-09-989-735-262
; Sequence 262, Application US/09989735
; Patent No. 697185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 461; DB 2; Length 89;

Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERVTLALLLLAGLTALRANDPFANKDDPFYDWNQLSLGICGGLAIAAGIAVLGSK 60

Db 1 MERVTLALLLLAGLTALRANDPFANKDDPFYDWNQLSLGICGGLAIAAGIAVLGSK 60

Qy 61 CKYSSQKHSPVPEKAIPITPGSATTC 89

Db 61 CKYSSQKHSPVPEKAIPITPGSATTC 89

RESULT 5

US-09-992-598-262

; Sequence 262, Application US/09992598

; Patent No. 6956108

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumaas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC27
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;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 461; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERVTLALLLGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAAGIAAVLSGK 60
Db 1 MERVTLALLLGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAAGIAAVLSGK 60

QY 61 CRYKSSQKQHSVPPEKAIPLIITPGSATTC 89
Db 61 CRYKSSQKQHSVPPEKAIPLIITPGSATTC 89

RESULT 3
US-09-990-444-262
; Sequence 262, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.

;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PLC19
;; CURRENT APPLICATION NUMBER: US/09/990,444
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
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;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088738
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088742

APPLICANT: Gurney,Austin L.
APPLICANT: Kljavin,Ivar J.
APPLICANT: Napier,Mary A.
APPLICANT: Pan,James
APPLICANT: Paoni,Nicholas F.
APPLICANT: Roy,Margaret Ann
APPLICANT: Stewart,Timothy A.
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APPLICANT: Zhang,Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR APPLICATION NUMBER: 60/090540

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1426	48	10.4	192	2	US-09-704-640-87	Sequence 87, Appl	1499	48	10.4	453	2	US-09-252-991A-20755	Sequence 20755, A
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ALIGNMENTS

RESULT 1
US-09-289-349-11
; Sequence 11, Application US/09289349
; Patent No. 6277574
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; APPLICANT: Volkumuth, Wayne
; APPLICANT: Klingner, Todd, M.
; APPLICANT: Azimzai, Yalda
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY
; FILE REFERENCE: PB-0010 US
; CURRENT APPLICATION NUMBER: US/09/289,349
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1900433CD1
US-09-289-349-11

Query Match 100.0%; Score 461; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 262, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

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1293	48.5	10.5	114	2	US-09-938-936-4	Sequence 4, Appli	1366	48.5	10.5	511	2	US-09-679-686B-12	Sequence 12, Appl
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1303	48.5	10.5	114	2	US-10-053-406-9	Sequence 9, Appli	1376	48.5	10.5	608	2	US-09-769-787-8	Sequence 8, Appli
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1309	48.5	10.5	114	2	US-10-053-406-15	Sequence 15, Appl	1382	48.5	10.5	684	2	US-09-252-991A-24618	Sequence 24618, A
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1312	48.5	10.5	114	2	US-10-053-406-18	Sequence 18, Appl	1385	48.5	10.5	815	2	US-09-489-039A-12469	Sequence 12469, A
1313	48.5	10.5	114	2	US-10-053-406-19	Sequence 19, Appl	1386	48.5	10.5	825	2	US-09-489-039A-8469	Sequence 8469, Ap
1314	48.5	10.5	114	2	US-10-053-406-20	Sequence 20, Appl	1387	48.5	10.5	938	2	US-09-637-145-2	Sequence 2, Appli
1315	48.5	10.5	114	2	US-10-053-406-21	Sequence 21, Appl	1388	48.5	10.5	1052	2	US-09-949-016-11508	Sequence 11508, A
1316	48.5	10.5	114	2	US-10-053-406-22	Sequence 22, Appl	1389	48.5	10.5	1161	2	US-09-327-536-2	Sequence 2, Appli
1317	48.5	10.5	132	1	US-08-012-543-2	Sequence 2, Appli	1390	48.5	10.5	1278	2	US-09-134-000C-6043	Sequence 6043, Ap
1318	48.5	10.5	132	2	US-09-054-711C-3	Sequence 3, Appli	1391	48.5	10.5	1501	1	US-08-447-464-3	Sequence 3, Appli
1319	48.5	10.5	132	2	US-09-462-941-19	Sequence 19, Appl	1392	48.5	10.5	1501	1	US-08-716-679-3	Sequence 3, Appli
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1321	48.5	10.5	132	5	PCT-US93-07645A-2	Sequence 2, Appli	1394	48.5	10.5	4545	1	US-08-804-227C-14	Sequence 14, Appl
1322	48.5	10.5	132	5	PCT-US93-07645-2	Sequence 2, Appli	1395	48.5	10.5	4550	1	US-08-804-227C-8	Sequence 8, Appli
1323	48.5	10.5	136	2	US-09-378-238-33	Sequence 33, Appl	1396	48.5	10.5	4550	1	US-08-804-198-2	Sequence 2, Appli
1324	48.5	10.5	136	2	US-09-626-896-29	Sequence 29, Appl	1397	48	10.4	21	3	US-09-502-698-72	Sequence 72, Appl
1325	48.5	10.5	136	2	US-09-841-730-29	Sequence 29, Appl	1398	48	10.4	28	2	US-09-962-756-1457	Sequence 1457, Ap
1326	48.5	10.5	137	2	US-09-270-767-31676	Sequence 31676, A	1399	48	10.4	70	2	US-09-252-991A-16917	Sequence 16917, A
1327	48.5	10.5	137	2	US-09-949-016-6187	Sequence 19, Appl	1400	48	10.4	72	2	US-09-312-283C-182	Sequence 182, App
1328	48.5	10.5	150	2	US-09-949-016-6187	Sequence 19, Appl	1401	48	10.4	73	2	US-09-489-847-300	Sequence 300, App
1329	48.5	10.5	157	2	US-09-378-238-31	Sequence 31, Appl	1402	48	10.4	74	2	US-09-489-847-229	Sequence 229, App
1330	48.5	10.5	157	2	US-09-626-896-27	Sequence 27, Appl	1403	48	10.4	76	2	US-09-962-756-2182	Sequence 2182, Ap
1331	48.5	10.5	157	2	US-09-841-730-27	Sequence 27, Appl	1404	48	10.4	86	2	US-10-002-344A-186	Sequence 186, App
1332	48.5	10.5	198	2	US-09-489-039A-7760	Sequence 7760, Ap	1405	48	10.4	120	2	US-09-931-381A-12	Sequence 12, Appl
1333	48.5	10.5	217	2	US-09-252-991A-30489	Sequence 30489, A	1406	48	10.4	120	2	US-09-513-999C-4290	Sequence 4290, Ap
1334	48.5	10.5	219	2	US-09-248-796A-19579	Sequence 19579, A	1407	48	10.4	120	2	US-09-898-751A-14	Sequence 14, Appl
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1336	48.5	10.5	247	1	US-07-885-089B-8	Sequence 8, Appli	1409	48	10.4	133	2	US-10-206-576-226	Sequence 226, App
1337	48.5	10.5	256	2	US-09-198-452A-449	Sequence 449, App	1410	48	10.4	136	2	US-09-489-039A-10864	Sequence 10864, A
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1339	48.5	10.5	257	2	US-09-438-185A-432	Sequence 432, App	1412	48	10.4	136	2	US-09-270-767-47000	Sequence 47000, A
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1125	49	10.6	118	2	US-09-056-556-231	Sequence 231, App	1198	49	10.6	405	2	US-09-252-991A-19717	Sequence 19717, A
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1148	49	10.6	239	2	US-08-913-014A-3	Sequence 3, Appli	1221	49	10.6	659	2	US-09-228-986-75	Sequence 75, Appl
1149	49	10.6	239	2	US-09-653-285-3	Sequence 3, Appli	1222	49	10.6	677	2	US-10-101-464A-75	Sequence 75, Appl
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1156	49	10.6	266	2	US-09-134-000C-3847	Sequence 3847, Ap	1229	49	10.6	740	2	US-09-248-796A-17362	Sequence 17362, A
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1158	49	10.6	282	2	US-09-385-442-7	Sequence 7, Appli	1231	49	10.6	785	2	US-09-949-016-11569	Sequence 11569, A
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1162	49	10.6	337	2	US-08-765-961-1	Sequence 1, Appli	1235	49	10.6	908	2	US-09-328-352-5527	Sequence 5527, Ap
1163	49	10.6	331	2	US-08-765-961-1	Sequence 1, Appli	1236	49	10.6	908	2	US-09-635-877A-15	Sequence 15, Appl
1164	49	10.6	332	2	US-09-328-352-4745	Sequence 4745, Ap	1237	49	10.6	908	2	US-09-636-060C-15	Sequence 15, Appl
1165	49	10.6	342	2	US-08-785-928-1	Sequence 1, Appli	1238	49	10.6	908	2	US-09-986-552-15	Sequence 15, Appl
1166	49	10.6	342	2	US-08-728-603-17	Sequence 17, Appl	1239	49	10.6	908	2	US-09-636-596C-15	Sequence 15, Appl
1167	49	10.6	345	2	US-09-328-352-4841	Sequence 4841, Ap	1240	49	10.6	908	2	US-10-023-894-9	Sequence 9, Appli
1168	49	10.6	345	2	US-10-094-749-3021	Sequence 3021, Ap	1241	49	10.6	908	2	US-10-306-686-15	Sequence 15, Appl
1169	49	10.6	349	2	US-08-630-172-6	Sequence 6, Appli	1242	49	10.6	908	2	US-09-895-072-15	Sequence 15, Appl
1170	49	10.6	349	2	US-09-375-419-6	Sequence 6, Appli	1243	49	10.6	914	2	US-10-023-888-9	Sequence 9, Appli
1171	49	10.6	349	2	US-09-134-001C-4004	Sequence 4004, Ap	1244	49	10.6	914	2	US-09-193-562D-28	Sequence 28, Appl
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1173	49	10.6	352	2	US-09-087-232A-13	Sequence 13, Appl	1246	49	10.6	914	2	US-10-053-412B-28	Sequence 28, Appl
1174	49	10.6	352	2	US-08-861-105-14	Sequence 14, Appl	1247	49	10.6	914	2	US-10-270-595-6	Sequence 6, Appli
1175	49	10.6	352	2	US-08-575-967A-2	Sequence 2, Appli	1248	49	10.6	946	2	US-09-902-540-16817	Sequence 16817, A
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1177	49	10.6	352	2	US-09-517-605-5	Sequence 5, Appli	1250	49	10.6	1070	1	US-08-633-770A-2	Sequence 2, Appli
1178	49	10.6	352	2	US-09-534-185-52	Sequence 52, Appl	1251	49	10.6	1070	2	US-09-280-197-6	Sequence 6, Appli
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1183	49	10.6	352	2	US-09-502-784A-2	Sequence 2, Appli	1256	49	10.6	1200	2	US-10-094-749-2682	Sequence 2682, Ap
1184	49	10.6	352	2	US-09-339-912A-2	Sequence 2, Appli	1257	49	10.6	1956	2	US-10-152-886-23	Sequence 23, Appl
1185	49	10.6	352	2	US-08-771-276-2	Sequence 2, Appli	1258	48.5	10.5	27	2	US-09-962-756-1637	Sequence 1637, Ap
1186	49	10.6	352	2	US-08-771-276-20	Sequence 20, Appl	1259	48.5	10.5	51	1	US-10-067-422-18	Sequence 18, Appl
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1189	49	10.6	352	2	US-09-949-002-303	Sequence 303, App	1262	48.5	10.5	77	2	US-08-311-731A-385	Sequence 385, App
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1191	49	10.6	352	2	US-09-938-703B-5	Sequence 5, Appli	1264	48.5	10.5	112	1	US-08-284-393B-4	Sequence 4, Appli
1192	49	10.6	352	2	US-10-072-301A-1	Sequence 1, Appli	1265	48.5	10.5	112	1	US-08-284-393B-14	Sequence 14, Appl
1193	49	10.6	357	2	US-09-949-016-9074	Sequence 9074, Ap	1266	48.5	10.5	112	5	PCT-US95-08950-4	Sequence 4, Appli
1194	49	10.6	358	2	US-09-543-681A-4765	Sequence 4765, Ap	1267	48.5	10.5	114	2	US-09-054-711C-4	Sequence 4, Appli

976	50	10.8	501	2	US-09-252-991A-31885	Sequence 31885, A	1049	49.5	10.7	394	2	US-09-710-279-3292	Sequence 3292, Ap
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978	50	10.8	525	2	US-09-949-016-7407	Sequence 7407, Ap	1051	49.5	10.7	414	2	US-09-710-279-806	Sequence 806, App
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981	50	10.8	605	2	US-09-949-016-8269	Sequence 8269, A	1054	49.5	10.7	427	2	US-09-328-352-6602	Sequence 6602, Ap
982	50	10.8	606	2	US-09-538-092-798	Sequence 798, App	1055	49.5	10.7	432	2	US-09-902-540-9717	Sequence 9717, Ap
983	50	10.8	641	2	US-09-653-274-13	Sequence 13, Appl	1056	49.5	10.7	436	2	US-09-886-319A-72	Sequence 72, Appl
984	50	10.8	641	2	US-10-461-791-13	Sequence 13, Appl	1057	49.5	10.7	462	2	US-08-753-007A-8	Sequence 8, Appli
985	50	10.8	772	2	US-09-252-991A-30446	Sequence 30446, A	1058	49.5	10.7	469	2	US-09-398-496-8	Sequence 8, Appli
986	50	10.8	970	2	US-09-979-195-10	Sequence 10, Appl	1059	49.5	10.7	470	2	US-10-104-047-3775	Sequence 3775, Ap
987	50	10.8	1070	2	US-09-653-274-8	Sequence 8, Appli	1060	49.5	10.7	476	2	US-09-134-001C-3778	Sequence 3778, Ap
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990	50	10.8	1309	2	US-10-461-791-4	Sequence 4, Appli	1063	49.5	10.7	507	2	US-10-214-811-2	Sequence 2, Appli
991	50	10.8	1309	2	US-09-862-027-82	Sequence 82, Appli	1064	49.5	10.7	507	2	US-10-766-074-2	Sequence 2, Appli
992	50	10.8	1381	2	US-08-826-134-4	Sequence 4, Appli	1065	49.5	10.7	532	2	US-09-780-016-20	Sequence 20, Appl
993	50	10.8	1443	1	US-08-308-872B-2	Sequence 2, Appli	1066	49.5	10.7	532	2	US-10-214-811-20	Sequence 20, Appl
994	50	10.8	1479	2	US-08-840-062-2	Sequence 2, Appli	1067	49.5	10.7	532	2	US-10-766-074-20	Sequence 20, Appl
995	49.5	10.7	58	1	US-08-721-745-2	Sequence 2, Appli	1068	49.5	10.7	556	2	US-09-907-794A-259	Sequence 259, App
996	49.5	10.7	59	2	US-09-513-999C-5346	Sequence 6346, Ap	1069	49.5	10.7	556	2	US-09-905-125A-259	Sequence 259, App
997	49.5	10.7	66	2	US-09-513-999C-7224	Sequence 7224, Ap	1070	49.5	10.7	556	2	US-09-902-775A-259	Sequence 259, App
998	49.5	10.7	160	2	US-09-732-210-304	Sequence 304, App	1071	49.5	10.7	556	2	US-09-906-700-259	Sequence 259, App
999	49.5	10.7	160	2	US-09-107-532A-5111	Sequence 5111, Ap	1072	49.5	10.7	556	2	US-09-903-603A-259	Sequence 259, App
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1001	49.5	10.7	172	2	US-09-062-126-2	Sequence 2, Appli	1074	49.5	10.7	556	2	US-09-909-064-259	Sequence 259, App
1002	49.5	10.7	193	2	US-09-475-316A-78	Sequence 78, Appl	1075	49.5	10.7	556	2	US-09-905-381A-259	Sequence 259, App
1003	49.5	10.7	193	2	US-09-704-640-78	Sequence 78, Appl	1076	49.5	10.7	556	2	US-09-906-618-259	Sequence 259, App
1004	49.5	10.7	200	1	US-08-698-805-6	Sequence 6, Appli	1077	49.5	10.7	556	2	US-09-906-646-259	Sequence 259, App
1005	49.5	10.7	212	2	US-09-813-453B-59	Sequence 59, Appl	1078	49.5	10.7	556	2	US-09-904-462-259	Sequence 259, App
1006	49.5	10.7	226	2	US-10-094-749-2249	Sequence 2249, Ap	1079	49.5	10.7	556	2	US-09-902-736A-259	Sequence 259, App
1007	49.5	10.7	246	2	US-09-134-001C-5292	Sequence 5292, Ap	1080	49.5	10.7	556	2	US-09-906-722A-259	Sequence 259, App
1008	49.5	10.7	249	1	US-08-626-685A-11	Sequence 11, Appl	1081	49.5	10.7	556	2	US-09-905-449-259	Sequence 259, App
1009	49.5	10.7	249	2	US-09-248-796A-19210	Sequence 19210, A	1082	49.5	10.7	556	2	US-09-903-562B-259	Sequence 259, App
1010	49.5	10.7	252	1	US-07-885-089B-7	Sequence 7, Appli	1083	49.5	10.7	556	2	US-09-906-679A-259	Sequence 259, App
1011	49.5	10.7	252	2	US-09-976-594-582	Sequence 582, App	1084	49.5	10.7	556	3	US-09-907-841-259	Sequence 259, App
1012	49.5	10.7	252	2	US-09-919-039-228	Sequence 228, App	1085	49.5	10.7	557	2	US-10-771-708-4	Sequence 4, Appli
1013	49.5	10.7	262	2	US-09-134-001C-3746	Sequence 3746, Ap	1086	49.5	10.7	563	2	US-08-931-608A-3	Sequence 3, Appli
1014	49.5	10.7	262	2	US-09-710-279-1568	Sequence 1568, Ap	1087	49.5	10.7	563	2	US-08-851-847-3	Sequence 3, Appli
1015	49.5	10.7	265	2	US-09-780-016-8	Sequence 8, Appli	1088	49.5	10.7	582	2	US-09-252-991A-21510	Sequence 21510, A
1016	49.5	10.7	265	2	US-10-214-811-8	Sequence 8, Appli	1089	49.5	10.7	597	2	US-09-252-991A-32657	Sequence 32657, A
1017	49.5	10.7	265	2	US-10-766-074-8	Sequence 8, Appli	1090	49.5	10.7	607	2	US-09-252-991A-32643	Sequence 32643, A
1018	49.5	10.7	268	2	US-09-716-964B-156	Sequence 156, App	1091	49.5	10.7	637	2	US-09-569-611C-35	Sequence 35, Appl
1019	49.5	10.7	290	2	US-09-780-016-6	Sequence 6, Appli	1092	49.5	10.7	637	2	US-08-753-007A-32	Sequence 32, Appl
1020	49.5	10.7	290	2	US-10-214-811-6	Sequence 6, Appli	1093	49.5	10.7	647	2	US-08-398-456-32	Sequence 32, Appl
1021	49.5	10.7	290	2	US-10-766-074-6	Sequence 6, Appli	1094	49.5	10.7	660	2	US-09-907-794A-28	Sequence 28, Appl
1022	49.5	10.7	296	2	US-09-489-847-293	Sequence 293, App	1095	49.5	10.7	660	2	US-09-905-125A-28	Sequence 28, Appl
1023	49.5	10.7	315	2	US-09-107-532A-28066	Sequence 28066, A	1096	49.5	10.7	660	2	US-09-902-775A-28	Sequence 28, Appl
1024	49.5	10.7	319	2	US-09-252-991A-28066	Sequence 28066, A	1097	49.5	10.7	660	2	US-09-906-700-28	Sequence 28, Appl
1025	49.5	10.7	320	2	US-09-489-039A-10349	Sequence 10349, A	1098	49.5	10.7	660	2	US-09-903-603A-28	Sequence 28, Appl
1026	49.5	10.7	322	2	US-09-949-016-11381	Sequence 11381, A	1099	49.5	10.7	660	2	US-09-904-920A-28	Sequence 28, Appl
1027	49.5	10.7	324	2	US-09-602-787A-484	Sequence 484, App	1100	49.5	10.7	660	2	US-09-949-016-6843	Sequence 6843, Ap
1028	49.5	10.7	328	2	US-09-605-703B-2840	Sequence 2840, Ap	1101	49.5	10.7	660	2	US-09-909-064-28	Sequence 28, Appl
1029	49.5	10.7	353	2	US-09-489-039A-12270	Sequence 12270, A	1102	49.5	10.7	660	2	US-09-905-381A-28	Sequence 28, Appl
1030	49.5	10.7	363	2	US-09-949-016-11040	Sequence 11040, A	1103	49.5	10.7	660	2	US-09-906-618-28	Sequence 28, Appl
1031	49.5	10.7	364	2	US-09-489-039A-10066	Sequence 10066, A	1104	49.5	10.7	660	2	US-09-906-646-28	Sequence 28, Appl
1032	49.5	10.7	372	1	US-08-626-685A-8	Sequence 8, Appli	1105	49.5	10.7	660	2	US-09-689-486-58	Sequence 58, Appl
1033	49.5	10.7	372	2	US-08-993-088A-2	Sequence 2, Appli	1106	49.5	10.7	660	2	US-09-904-462-28	Sequence 28, Appl
1034	49.5	10.7	372	2	US-08-993-088A-20	Sequence 20, Appli	1107	49.5	10.7	660	2	US-09-902-736A-28	Sequence 28, Appl
1035	49.5	10.7	372	2	US-08-993-424B-2	Sequence 2, Appli	1108	49.5	10.7	660	2	US-09-906-722A-28	Sequence 28, Appl
1036	49.5	10.7	372	2	US-08-665-034A-2	Sequence 2, Appli	1109	49.5	10.7	660	2	US-09-905-449-28	Sequence 28, Appl
1037	49.5	10.7	372	2	US-08-665-034A-4	Sequence 4, Appli	1110	49.5	10.7	660	2	US-09-903-562B-28	Sequence 28, Appl
1038	49.5	10.7	372	2	US-09-595-549-9	Sequence 9, Appli	1111	49.5	10.7	660	2	US-09-905-679A-28	Sequence 28, Appl
1039	49.5	10.7	372	2	US-09-603-680-2	Sequence 2, Appli	1112	49.5	10.7	660	2	US-09-973-424A-58	Sequence 58, Appl
1040	49.5	10.7	372	2	US-08-603-680-20	Sequence 20, Appli	1113	49.5	10.7	661	3	US-09-907-841-28	Sequence 28, Appl
1041	49.5	10.7	372	2	US-09-981-700A-2	Sequence 2, Appli	1114	49.5	10.7	661	2	US-09-252-991A-27070	Sequence 27070, A
1042	49.5	10.7	372	2	US-08-899-112B-8	Sequence 8, Appli	1115	49.5	10.7	662	2	US-09-902-540-12594	Sequence 12594, Ap
1043	49.5	10.7	372	2	US-09-011-553-2	Sequence 2, Appli	1116	49.5	10.7	683	2	US-09-945-016-7267	Sequence 7267, Ap
1044	49.5	10.7	378	2	US-09-689-486-62	Sequence 62, Appli	1117	49.5	10.7	741	2	US-09-252-991A-22440	Sequence 22440, A
1045	49.5	10.7	378	2	US-09-973-424A-62	Sequence 62, Appl	1118	49.5	10.7	770	2	US-09-538-092-1265	Sequence 1265, Ap
1046	49.5	10.7	380	2	US-09-120-365-76	Sequence 76, Appl	1119	49.5	10.7	1121	2	US-08-915-048A-2	Sequence 2, Appli
1047	49.5	10.7	380	2	US-09-515-039-76	Sequence 76, Appl	1120	49.5	10.7	2446	2	US-09-949-016-11439	Sequence 11439, A
1048	49.5	10.7	380	2	US-08-860-255A-5	Sequence 5, Appli	1121	49	10.6	63	2	US-09-471-276-1429	Sequence 1429, Ap

830	51	11.1	1093	2	US-09-854-845-4	Sequence 4, Appli	903	50.5	11.0	1163	1	US-08-482-293A-4	Sequence 4, Appli
831	51	11.1	1151	2	US-09-854-845-10	Sequence 10, Appl	904	50.5	11.0	1163	1	US-08-943-363-4	Sequence 4, Appli
832	51	11.1	1479	2	US-08-840-062-4	Sequence 4, Appli	905	50.5	11.0	1163	1	US-08-476-062A-44	Sequence 44, Appl
833	51	11.1	1956	2	US-08-843-417-10	Sequence 10, Appl	906	50.5	11.0	1163	2	US-08-193-043-4	Sequence 4, Appli
834	51	11.1	1956	2	US-09-527-013-10	Sequence 10, Appl	907	50.5	11.0	1163	2	US-09-688-307A-4	Sequence 4, Appli
835	50.5	11.0	26	2	US-09-962-756-1658	Sequence 1658, Ap	908	50.5	11.0	1163	2	US-09-350-259-4	Sequence 44, Appl
836	50.5	11.0	87	2	US-09-605-703B-960	Sequence 960, App	909	50.5	11.0	1163	5	PCT-US96-01314-44	Sequence 5, Appli
837	50.5	11.0	87	2	US-09-605-703B-962	Sequence 962, App	910	50.5	11.0	1211	2	US-09-491-522-5	Sequence 5, Appli
838	50.5	11.0	142	2	US-10-104-047-2706	Sequence 2706, Ap	911	50.5	11.0	1211	2	US-09-949-016-11401	Sequence 11401, A
839	50.5	11.0	147	2	US-09-543-681A-4506	Sequence 4506, Ap	912	50.5	11.0	1211	2	US-09-949-002-401	Sequence 401, App
840	50.5	11.0	188	1	US-08-160-524A-5	Sequence 5, Appli	913	50.5	11.0	1211	2	US-09-949-002-555	Sequence 555, App
841	50.5	11.0	207	1	US-08-609-443B-15	Sequence 15, Appl	914	50.5	11.0	1245	2	US-09-252-921A-30935	Sequence 30935, A
842	50.5	11.0	207	1	US-08-569-063C-15	Sequence 15, Appl	915	50.5	11.0	1317	2	US-09-083-521-7	Sequence 7, Appli
843	50.5	11.0	207	2	US-08-851-896-15	Sequence 15, Appl	916	50.5	11.0	2703	1	US-08-185-232-19	Sequence 19, Appl
844	50.5	11.0	249	2	US-09-583-110-4357	Sequence 4357, Ap	917	50.5	11.0	2703	2	US-08-899-232-4	Sequence 4, Appli
845	50.5	11.0	249	2	US-09-602-777A-344	Sequence 344, App	918	50.5	11.0	2703	2	US-08-121-457-4	Sequence 4, Appli
846	50.5	11.0	254	2	US-09-107-433-4333	Sequence 4333, Ap	919	50.5	11.0	3169	1	US-08-477-451-6	Sequence 6, Appli
847	50.5	11.0	255	2	US-09-605-703B-244	Sequence 244, App	920	50.5	11.0	31	2	US-09-270-767-52626	Sequence 37409, A
848	50.5	11.0	263	2	US-09-605-703B-242	Sequence 242, App	921	50.5	10.8	31	2	US-09-248-796A-27038	Sequence 52626, A
849	50.5	11.0	264	1	US-08-463-115-93	Sequence 93, Appl	922	50.5	10.8	92	2	US-09-127-946-8	Sequence 8, Appli
850	50.5	11.0	264	1	US-08-465-388-93	Sequence 93, Appl	923	50.5	10.8	92	2	US-09-148-545-256	Sequence 256, App
851	50.5	11.0	271	2	US-09-252-991A-18965	Sequence 18965, A	924	50.5	10.8	93	2	US-09-621-011-256	Sequence 256, App
852	50.5	11.0	304	2	US-09-502-540-13353	Sequence 13353, A	925	50.5	10.8	93	2	US-09-198-452A-475	Sequence 475, App
853	50.5	11.0	306	2	US-09-252-991A-22181	Sequence 22181, A	926	50.5	10.8	102	2	US-09-248-796A-19711	Sequence 19711, A
854	50.5	11.0	326	2	US-09-328-352-5506	Sequence 5506, Ap	927	50.5	10.8	105	2	US-09-482-273-264	Sequence 264, App
855	50.5	11.0	349	2	US-09-949-016-9786	Sequence 9786, Ap	928	50.5	10.8	119	2	US-09-482-273-264	Sequence 264, App
856	50.5	11.0	355	2	US-08-984-618-14	Sequence 14, Appl	929	50.5	10.8	147	2	US-09-902-540-12970	Sequence 12970, A
857	50.5	11.0	364	2	US-09-829-275-1	Sequence 1, Appli	930	50.5	10.8	147	2	US-09-394-142B-16	Sequence 16, Appl
858	50.5	11.0	377	1	US-08-188-277B-2	Sequence 2, Appli	931	50.5	10.8	201	2	US-09-270-767-31650	Sequence 31650, A
859	50.5	11.0	377	1	US-08-429-964-80	Sequence 80, Appl	932	50.5	10.8	201	2	US-09-270-767-46867	Sequence 46867, A
860	50.5	11.0	385	2	US-09-107-532A-5871	Sequence 5871, Ap	933	50.5	10.8	201	2	US-10-094-749-3240	Sequence 3240, Ap
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862	50.5	11.0	424	2	US-09-302-540-10575	Sequence 10575, A	935	50.5	10.8	252	2	US-09-502-540-12546	Sequence 12546, A
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864	50.5	11.0	433	2	US-09-502-540-13296	Sequence 13296, A	937	50.5	10.8	263	2	US-09-328-352-4486	Sequence 4486, App
865	50.5	11.0	442	2	US-09-538-092-637	Sequence 637, App	938	50.5	10.8	264	2	US-09-198-452A-266	Sequence 266, App
866	50.5	11.0	455	2	US-09-543-681A-7043	Sequence 7043, Ap	939	50.5	10.8	267	2	US-09-134-000C-6206	Sequence 6206, Ap
867	50.5	11.0	461	2	US-09-107-532A-5964	Sequence 5964, Ap	940	50.5	10.8	272	2	US-09-489-039A-12374	Sequence 12374, A
868	50.5	11.0	467	2	US-09-302-540-11298	Sequence 11298, A	941	50.5	10.8	277	2	US-09-303-518D-400	Sequence 400, App
869	50.5	11.0	476	2	US-10-142-835-28	Sequence 28, Appl	942	50.5	10.8	279	2	US-09-134-001C-4878	Sequence 4878, Ap
870	50.5	11.0	477	2	US-09-252-991A-29825	Sequence 29825, A	943	50.5	10.8	303	2	US-09-543-681A-5154	Sequence 5154, Ap
871	50.5	11.0	499	2	US-09-252-991A-27221	Sequence 27221, A	944	50.5	10.8	308	1	US-08-164-292B-18	Sequence 18, Appl
872	50.5	11.0	529	1	US-07-891-942C-8	Sequence 8, Appli	945	50.5	10.8	308	2	US-08-845-623-18	Sequence 18, Appl
873	50.5	11.0	529	1	US-08-370-909-19	Sequence 19, Appl	946	50.5	10.8	308	2	US-08-815-927-18	Sequence 18, Appl
874	50.5	11.0	529	1	US-08-504-048-8	Sequence 8, Appli	947	50.5	10.8	308	2	US-09-103-330-18	Sequence 18, Appl
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876	50.5	11.0	529	2	US-09-169-717B-39	Sequence 39, Appl	949	50.5	10.8	308	3	US-10-046-938-18	Sequence 18, Appl
877	50.5	11.0	529	2	US-10-011-436-4	Sequence 4, Appli	950	50.5	10.8	322	2	US-09-252-991A-24657	Sequence 24657, A
878	50.5	11.0	529	2	US-08-533-895A-39	Sequence 39, Appl	951	50.5	10.8	323	2	US-09-107-532A-6263	Sequence 6263, Ap
879	50.5	11.0	529	3	US-08-816-454B-232	Sequence 232, App	952	50.5	10.8	326	2	US-09-784-810C-11	Sequence 11, Appl
880	50.5	11.0	537	2	US-08-540-922D-12	Sequence 12, Appl	953	50.5	10.8	351	2	US-10-099-322-100	Sequence 100, App
881	50.5	11.0	550	1	US-08-279-700-18	Sequence 18, Appl	954	50.5	10.8	351	2	US-10-044-564-100	Sequence 100, App
882	50.5	11.0	550	1	US-08-279-700-20	Sequence 20, Appl	955	50.5	10.8	356	2	US-09-125-619-2	Sequence 2, Appli
883	50.5	11.0	550	1	US-08-279-700-22	Sequence 22, Appl	956	50.5	10.8	356	2	US-09-125-619-13	Sequence 13, Appl
884	50.5	11.0	560	1	US-07-891-942C-5	Sequence 5, Appli	957	50.5	10.8	356	2	US-10-222-566-2	Sequence 2, Appli
885	50.5	11.0	566	2	US-09-491-522-7	Sequence 7, Appli	958	50.5	10.8	356	2	US-10-222-566-13	Sequence 13, Appl
886	50.5	11.0	566	2	US-09-949-016-7010	Sequence 7010, Ap	959	50.5	10.8	356	2	US-10-143-024A-2	Sequence 2, Appli
887	50.5	11.0	566	2	US-09-949-016-8505	Sequence 8505, Ap	960	50.5	10.8	356	2	US-10-143-024A-13	Sequence 13, Appl
888	50.5	11.0	566	2	US-09-949-002-452	Sequence 452, App	961	50.5	10.8	356	2	US-10-222-162-2	Sequence 2, Appli
889	50.5	11.0	572	2	US-10-154-419-13	Sequence 13, Appl	962	50.5	10.8	356	2	US-10-222-162-13	Sequence 13, Appl
890	50.5	11.0	585	3	US-09-622-964A-3	Sequence 3, Appli	963	50.5	10.8	358	2	US-09-270-767-45037	Sequence 45037, A
891	50.5	11.0	596	2	US-09-252-991A-22689	Sequence 22689, A	964	50.5	10.8	378	2	US-09-902-540-11860	Sequence 11860, A
892	50.5	11.0	614	2	US-09-949-016-10772	Sequence 10772, A	965	50.5	10.8	390	2	US-09-710-279-1422	Sequence 1422, Ap
893	50.5	11.0	757	2	US-09-902-540-11380	Sequence 11380, A	966	50.5	10.8	427	2	US-09-502-540-15413	Sequence 15413, A
894	50.5	11.0	867	2	US-09-839-894-6	Sequence 6, Appli	967	50.5	10.8	436	2	US-08-584-760A-67	Sequence 67, Appl
895	50.5	11.0	974	2	US-08-328-291A-4	Sequence 4, Appli	968	50.5	10.8	440	2	US-08-584-760A-1	Sequence 1, Appli
896	50.5	11.0	974	2	US-09-589-619-4	Sequence 4, Appli	969	50.5	10.8	447	2	US-10-162-012-29	Sequence 29, Appl
897	50.5	11.0	1106	2	US-09-134-000C-6136	Sequence 6136, Ap	970	50.5	10.8	461	2	US-09-543-681A-6448	Sequence 6448, Ap
898	50.5	11.0	1163	1	US-08-173-497-4	Sequence 4, Appli	971	50.5	10.8	461	2	US-09-498-612-6	Sequence 6, Appli
899	50.5	11.0	1163	1	US-08-286-889-4	Sequence 4, Appli	972	50.5	10.8	468	3	US-09-497-967-7	Sequence 7, Appli
900	50.5	11.0	1163	1	US-08-485-618-4	Sequence 4, Appli	973	50.5	10.8	468	3	US-09-497-967-54	Sequence 54, Appl
901	50.5	11.0	1163	1	US-08-362-652-4	Sequence 4, Appli	974	50.5	10.8	468	3	US-09-784-810C-6	Sequence 6, Appli
902	50.5	11.0	1163	1	US-08-605-672-4	Sequence 4, Appli	975	50.5	10.8	471	2		

684	51.5	11.2	307	2	US-09-107-433-4181	Sequence 4181, Ap	757	51.5	11.2	1454	5	PCT-US93-04384-12	Sequence 12, Appl
685	51.5	11.2	307	2	US-10-012-231A-95	Sequence 95, Appl	758	51.5	11.2	1454	5	PCT-US93-04384-44	Sequence 44, Appl
686	51.5	11.2	307	2	US-10-015-389A-95	Sequence 95, Appl	759	51.5	11.2	1454	5	PCT-US93-04384-46	Sequence 46, Appl
687	51.5	11.2	307	2	US-10-006-768A-95	Sequence 95, Appl	760	51.5	11.2	1454	5	PCT-US93-04384-47	Sequence 47, Appl
688	51.5	11.2	307	2	US-10-015-671A-95	Sequence 95, Appl	761	51.5	11.2	2539	2	US-09-413-814-42	Sequence 42, Appl
689	51.5	11.2	307	2	US-10-015-393A-95	Sequence 95, Appl	762	51	11.1	86	2	US-08-654-737B-2	Sequence 2, Appl
690	51.5	11.2	307	2	US-10-011-833A-95	Sequence 95, Appl	763	51	11.1	109	2	US-09-198-452A-11	Sequence 11, Appl
691	51.5	11.2	307	2	US-10-006-041A-95	Sequence 95, Appl	764	51	11.1	109	2	US-09-438-185A-2	Sequence 2, Appl
692	51.5	11.2	307	2	US-10-012-064A-95	Sequence 95, Appl	765	51	11.1	119	2	US-09-270-767-32131	Sequence 32131, A
693	51.5	11.2	307	2	US-10-015-392A-95	Sequence 95, Appl	766	51	11.1	141	2	US-09-543-681A-6396	Sequence 6396, Ap
694	51.5	11.2	307	3	US-10-011-795B-95	Sequence 95, Appl	767	51	11.1	205	2	US-09-605-703B-1998	Sequence 1998, Ap
695	51.5	11.2	307	3	US-10-015-386A-95	Sequence 95, Appl	768	51	11.1	211	2	US-09-248-796A-20685	Sequence 20685, A
696	51.5	11.2	307	3	US-10-012-121A-95	Sequence 95, Appl	769	51	11.1	214	1	US-08-277-231A-14	Sequence 14, Appl
697	51.5	11.2	307	3	US-10-006-485A-95	Sequence 95, Appl	770	51	11.1	214	1	US-08-473-750-3	Sequence 3, Appl
698	51.5	11.2	307	3	US-10-006-746A-95	Sequence 95, Appl	771	51	11.1	214	1	US-08-477-326-3	Sequence 3, Appl
699	51.5	11.2	307	3	US-10-012-752A-95	Sequence 95, Appl	772	51	11.1	217	1	US-08-277-231A-2	Sequence 2, Appl
700	51.5	11.2	307	3	US-10-017-253A-95	Sequence 95, Appl	773	51	11.1	217	1	US-08-277-231A-12	Sequence 12, Appl
701	51.5	11.2	307	3	US-10-015-519A-95	Sequence 95, Appl	774	51	11.1	217	1	US-08-473-750-1	Sequence 1, Appl
702	51.5	11.2	307	3	US-10-015-715A-95	Sequence 95, Appl	775	51	11.1	217	1	US-08-473-750-5	Sequence 5, Appl
703	51.5	11.2	307	3	US-10-007-236A-95	Sequence 95, Appl	776	51	11.1	217	1	US-08-477-326-1	Sequence 1, Appl
704	51.5	11.2	319	2	US-08-581-148C-12	Sequence 12, Appl	777	51	11.1	217	1	US-08-477-326-5	Sequence 5, Appl
705	51.5	11.2	334	1	US-08-118-270-73	Sequence 73, Appl	778	51	11.1	222	2	US-09-252-991A-29014	Sequence 29014, A
706	51.5	11.2	334	5	PCT-US93-08528-73	Sequence 73, Appl	779	51	11.1	230	2	US-09-328-352-7370	Sequence 7370, Ap
707	51.5	11.2	362	3	US-09-993-844A-8	Sequence 8, Appl	780	51	11.1	294	2	US-09-252-991A-27242	Sequence 27242, A
708	51.5	11.2	369	1	US-08-416-756A-2	Sequence 2, Appl	781	51	11.1	301	2	US-09-489-039A-12748	Sequence 12748, A
709	51.5	11.2	369	2	US-08-880-865-2	Sequence 2, Appl	782	51	11.1	320	2	US-09-902-540-12563	Sequence 12563, A
710	51.5	11.2	371	2	US-09-949-016-9073	Sequence 9073, Ap	783	51	11.1	321	2	US-09-290-586A-22	Sequence 22, Appl
711	51.5	11.2	381	1	US-08-845-566-3	Sequence 3, Appl	784	51	11.1	321	3	US-10-329-258-18	Sequence 18, Appl
712	51.5	11.2	381	1	US-08-467-948A-28	Sequence 28, Appl	785	51	11.1	326	2	US-09-489-039A-11901	Sequence 11901, A
713	51.5	11.2	381	2	US-08-852-824-18	Sequence 18, Appl	786	51	11.1	328	2	US-09-489-039A-10986	Sequence 10986, A
714	51.5	11.2	381	2	US-08-467-947A-28	Sequence 28, Appl	787	51	11.1	330	2	US-09-134-001C-3815	Sequence 3815, Ap
715	51.5	11.2	381	2	US-09-731-030A-17	Sequence 17, Appl	788	51	11.1	338	2	US-09-949-016-8751	Sequence 8751, Ap
716	51.5	11.2	381	2	US-09-518-383-18	Sequence 18, Appl	789	51	11.1	346	2	US-08-888-429A-18	Sequence 18, Appl
717	51.5	11.2	381	5	PCT-US96-10618-4	Sequence 4, Appl	790	51	11.1	346	2	US-09-198-452A-60	Sequence 60, Appl
718	51.5	11.2	382	2	US-09-542-733-2	Sequence 2, Appl	791	51	11.1	354	2	US-09-593-653-18	Sequence 18, Appl
719	51.5	11.2	382	2	US-09-262-477-2	Sequence 2, Appl	792	51	11.1	361	1	US-09-902-540-15411	Sequence 15411, A
720	51.5	11.2	382	2	US-09-169-205D-21	Sequence 21, Appl	793	51	11.1	361	1	US-08-390-162-4	Sequence 4, Appl
721	51.5	11.2	383	1	US-08-196-989B-4	Sequence 4, Appl	794	51	11.1	361	1	US-08-685-945B-4	Sequence 4, Appl
722	51.5	11.2	383	1	US-08-760-936-4	Sequence 4, Appl	795	51	11.1	365	1	US-08-390-162-2	Sequence 2, Appl
723	51.5	11.2	383	2	US-09-225-024-4	Sequence 4, Appl	796	51	11.1	365	1	US-08-685-945B-2	Sequence 2, Appl
724	51.5	11.2	384	2	US-08-530-862B-4	Sequence 4, Appl	797	51	11.1	365	2	US-09-949-016-9075	Sequence 9075, Ap
725	51.5	11.2	384	2	US-08-597-313D-4	Sequence 4, Appl	798	51	11.1	370	2	US-09-489-039A-11515	Sequence 11515, A
726	51.5	11.2	384	2	US-09-885-189-4	Sequence 4, Appl	799	51	11.1	380	2	US-09-902-540-15775	Sequence 15775, A
727	51.5	11.2	390	1	US-08-416-756A-5	Sequence 5, Appl	800	51	11.1	383	2	US-08-530-862B-7	Sequence 7, Appl
728	51.5	11.2	390	2	US-08-880-865-5	Sequence 5, Appl	801	51	11.1	384	2	US-08-597-313D-7	Sequence 7, Appl
729	51.5	11.2	407	2	US-08-753-007A-6	Sequence 6, Appl	802	51	11.1	384	2	US-09-885-189-7	Sequence 7, Appl
730	51.5	11.2	407	2	US-09-398-496-6	Sequence 6, Appl	803	51	11.1	430	2	US-09-902-540-12684	Sequence 12684, A
731	51.5	11.2	429	2	US-08-311-731A-287	Sequence 287, App	804	51	11.1	438	2	US-09-107-532A-5677	Sequence 5677, Ap
732	51.5	11.2	453	2	US-09-540-236-3464	Sequence 3464, Ap	805	51	11.1	451	2	US-09-489-039A-8949	Sequence 8949, Ap
733	51.5	11.2	495	2	US-09-270-767-44726	Sequence 44726, A	806	51	11.1	475	2	US-09-489-039A-8862	Sequence 8862, Ap
734	51.5	11.2	509	2	US-08-845-546-2	Sequence 2, Appl	807	51	11.1	485	2	US-10-140-372-12	Sequence 12, Appl
735	51.5	11.2	511	2	US-09-252-991A-27306	Sequence 27306, A	808	51	11.1	485	2	US-09-438-185A-43	Sequence 43, Appl
736	51.5	11.2	522	2	US-09-549-519-40	Sequence 40, Appl	809	51	11.1	490	2	US-09-605-703B-1132	Sequence 1032, Ap
737	51.5	11.2	549	2	US-09-345-473E-32	Sequence 32, Appl	810	51	11.1	534	2	US-09-605-703B-1142	Sequence 1142, Ap
738	51.5	11.2	549	2	US-09-862-027-32	Sequence 32, Appl	811	51	11.1	584	2	US-09-107-532A-4564	Sequence 4564, Ap
739	51.5	11.2	550	1	US-08-348-891A-5	Sequence 5, Appl	812	51	11.1	590	2	US-09-248-796A-26874	Sequence 26874, A
740	51.5	11.2	550	1	US-08-905-817-5	Sequence 5, Appl	813	51	11.1	598	2	US-09-248-796A-19190	Sequence 19190, A
741	51.5	11.2	550	2	US-10-149-634-4	Sequence 4, Appl	814	51	11.1	677	2	US-09-252-991A-20406	Sequence 20406, A
742	51.5	11.2	563	2	US-10-046-232-24	Sequence 24, Appl	815	51	11.1	749	1	US-08-046-508-2	Sequence 2, Appl
743	51.5	11.2	567	2	US-09-252-991A-28481	Sequence 28481, A	816	51	11.1	749	2	US-09-250-083C-2	Sequence 2, Appl
744	51.5	11.2	586	2	US-09-489-039A-18033	Sequence 18033, A	817	51	11.1	822	2	US-09-248-796A-19917	Sequence 19917, A
745	51.5	11.2	630	2	US-09-252-991A-18033	Sequence 18033, A	818	51	11.1	866	1	US-08-386-727-8	Sequence 8, Appl
746	51.5	11.2	707	2	US-09-228-986-80	Sequence 80, Appl	819	51	11.1	866	1	US-08-600-452A-8	Sequence 8, Appl
747	51.5	11.2	707	2	US-10-101-464A-80	Sequence 80, Appl	820	51	11.1	954	2	US-09-854-845-14	Sequence 14, Appl
748	51.5	11.2	760	2	US-09-589-892B-11	Sequence 11, Appl	821	51	11.1	967	2	US-09-139-802-201	Sequence 201, App
749	51.5	11.2	808	2	US-10-104-047-2654	Sequence 10, Appl	822	51	11.1	967	2	US-09-659-786-201	Sequence 201, App
750	51.5	11.2	848	2	US-08-976-255-10	Sequence 10, Appl	823	51	11.1	967	2	US-10-095-322-14	Sequence 14, Appl
751	51.5	11.2	869	1	US-08-483-101-15	Sequence 15, Appl	824	51	11.1	967	2	US-10-095-322-74	Sequence 74, Appl
752	51.5	11.2	1204	2	US-10-094-749-2542	Sequence 2542, Ap	825	51	11.1	967	2	US-10-099-322-75	Sequence 75, Appl
753	51.5	11.2	1451	1	US-08-308-872B-4	Sequence 4, Appl	826	51	11.1	967	2	US-10-044-564-14	Sequence 14, Appl
754	51.5	11.2	1451	2	US-08-392-459-32	Sequence 32, Appl	827	51	11.1	967	2	US-10-044-564-74	Sequence 74, Appl
755	51.5	11.2	1454	2	US-09-854-799-32	Sequence 32, Appl	828	51	11.1	967	2	US-10-044-564-75	Sequence 75, Appl
756	51.5	11.2	1454	5	PCT-US91-08525-32	Sequence 32, Appl	829	51	11.1	1049	2	US-09-854-845-2	Sequence 2, Appl

538	52.5	11.4	410	2	US-09-078-596-2	Sequence 2, Appli	611	52	11.3	304	2	US-09-543-681A-7290	Sequence 7230, Ap
539	52.5	11.4	410	2	US-09-189-627A-11	Sequence 11, Appl	612	52	11.3	310	3	US-09-721-047A-4	Sequence 4, Appli
540	52.5	11.4	410	2	US-09-710-861-11	Sequence 11, Appl	613	52	11.3	312	2	US-09-543-681A-6689	Sequence 6689, Ap
541	52.5	11.4	435	2	US-09-489-039A-13740	Sequence 13740, A	614	52	11.3	316	2	US-09-902-540-10582	Sequence 10582, A
542	52.5	11.4	448	2	US-09-328-587-5807	Sequence 5807, Ap	615	52	11.3	350	2	US-09-543-681A-4618	Sequence 4618, Ap
543	52.5	11.4	468	2	US-09-602-787A-612	Sequence 612, App	616	52	11.3	371	2	US-09-949-016-8635	Sequence 8635, Ap
544	52.5	11.4	483	2	US-09-949-016-7773	Sequence 7773, Ap	617	52	11.3	380	2	US-08-888-429A-30	Sequence 30, Appl
545	52.5	11.4	523	2	US-09-538-092-571	Sequence 571, App	618	52	11.3	380	2	US-09-593-653-30	Sequence 30, Appl
546	52.5	11.4	523	2	US-08-888-949-16	Sequence 16, Appl	619	52	11.3	387	2	US-09-252-991A-22112	Sequence 22112, A
547	52.5	11.4	525	2	US-08-888-950-16	Sequence 16, Appl	620	52	11.3	389	2	US-08-888-429A-20	Sequence 20, Appl
548	52.5	11.4	525	2	US-09-262-758-16	Sequence 16, Appl	621	52	11.3	389	2	US-09-593-653-20	Sequence 20, Appl
549	52.5	11.4	525	2	US-09-885-876-16	Sequence 16, Appl	622	52	11.3	415	2	US-09-543-681A-6292	Sequence 6292, Ap
550	52.5	11.4	525	2	US-09-885-901-16	Sequence 16, Appl	623	52	11.3	419	2	US-08-888-429A-28	Sequence 28, Appl
551	52.5	11.4	525	2	US-09-731-393-16	Sequence 16, Appl	624	52	11.3	419	2	US-09-446-754-6	Sequence 6, Appli
552	52.5	11.4	550	2	US-09-120-365-1	Sequence 1, Appli	625	52	11.3	419	2	US-09-206-166-2	Sequence 2, Appli
553	52.5	11.4	550	2	US-09-515-039-1	Sequence 1, Appli	626	52	11.3	419	2	US-09-206-166-5	Sequence 5, Appli
554	52.5	11.4	551	3	US-09-622-964A-29	Sequence 29, Appl	627	52	11.3	419	2	US-09-593-653-28	Sequence 28, Appl
555	52.5	11.4	609	2	US-09-107-532A-5110	Sequence 5110, Ap	628	52	11.3	420	1	US-08-864-804-1	Sequence 1, Appli
556	52.5	11.4	693	2	US-09-949-016-9666	Sequence 9666, Ap	629	52	11.3	433	2	US-09-949-016-7636	Sequence 7636, Ap
557	52.5	11.4	706	2	US-09-252-991A-25730	Sequence 25730, A	630	52	11.3	435	2	US-09-446-754-2	Sequence 2, Appli
558	52.5	11.4	763	2	US-10-104-047-2766	Sequence 2766, Ap	631	52	11.3	453	2	US-08-888-429A-32	Sequence 32, Appl
559	52.5	11.4	763	3	US-09-502-698-88	Sequence 88, Appl	632	52	11.3	453	2	US-09-593-653-32	Sequence 32, Appl
560	52.5	11.4	800	2	US-09-489-039A-10358	Sequence 10358, A	633	52	11.3	468	2	US-09-446-754-4	Sequence 4, Appli
561	52.5	11.4	801	2	US-09-543-681A-7561	Sequence 7561, Ap	634	52	11.3	475	2	US-09-446-754-10	Sequence 10, Appl
562	52.5	11.4	969	2	US-09-321-987B-5	Sequence 5, Appli	635	52	11.3	475	2	US-09-949-016-11570	Sequence 11570, A
563	52.5	11.4	1000	2	US-09-352-159-25	Sequence 25, Appl	636	52	11.3	482	2	US-09-489-039A-9909	Sequence 9909, Ap
564	52.5	11.4	1000	2	US-09-352-168-25	Sequence 25, Appl	637	52	11.3	521	2	US-08-669-656A-4	Sequence 4, Appli
565	52.5	11.4	1000	2	US-09-771-045B-25	Sequence 25, Appl	638	52	11.3	596	2	US-09-134-001C-3363	Sequence 3363, Ap
566	52.5	11.4	1000	2	US-09-770-564A-25	Sequence 25, Appl	639	52	11.3	628	2	US-09-602-787A-550	Sequence 550, App
567	52.5	11.4	1000	2	US-09-658-835C-25	Sequence 25, Appl	640	52	11.3	628	2	US-09-602-787A-666	Sequence 666, App
568	52.5	11.4	1000	2	US-10-624-619A-25	Sequence 25, Appl	641	52	11.3	736	2	US-09-252-991A-19048	Sequence 19048, A
569	52.5	11.4	1005	3	US-09-502-698-2	Sequence 2, Appli	642	52	11.3	1194	2	US-09-949-016-9803	Sequence 9803, A
570	52.5	11.4	1101	2	US-08-331-625A-52	Sequence 52, Appl	643	52	11.3	1195	2	US-09-949-016-9803	Sequence 9803, A
571	52.5	11.4	1101	2	US-08-331-625A-54	Sequence 54, Appl	644	52	11.3	1195	2	US-09-949-016-9803	Sequence 9803, A
572	52.5	11.4	1101	2	US-09-494-151-52	Sequence 52, Appl	645	52	11.3	1956	2	US-08-843-417-2	Sequence 2, Appli
573	52.5	11.4	1101	2	US-09-494-151-54	Sequence 54, Appl	646	52	11.3	1957	2	US-09-527-013-2	Sequence 2, Appli
574	52.5	11.4	1101	2	US-09-972-484-52	Sequence 52, Appl	647	52	11.3	1957	2	US-08-669-656A-2	Sequence 2, Appli
575	52.5	11.4	1101	2	US-09-972-484-54	Sequence 54, Appl	648	52	11.3	1957	2	US-08-669-656A-8	Sequence 8, Appli
576	52.5	11.4	1205	2	US-09-491-522-11	Sequence 11, Appl	649	52	11.3	2057	2	US-08-478-853-19	Sequence 2, Appli
577	52.5	11.4	1279	2	US-09-489-039A-13602	Sequence 13602, A	650	52	11.3	2132	2	US-08-669-656A-6	Sequence 6, Appli
578	52.5	11.4	1373	3	US-09-502-698-1	Sequence 1, Appli	651	51.5	11.2	115	2	US-09-513-999C-7866	Sequence 7866, Ap
579	52.5	11.4	1452	2	US-08-331-625A-2	Sequence 2, Appli	652	51.5	11.2	123	1	US-08-180-209B-19	Sequence 19, Appl
580	52.5	11.4	1452	2	US-09-494-151-2	Sequence 2, Appli	653	51.5	11.2	123	1	US-08-385-745-19	Sequence 19, Appl
581	52.5	11.4	1452	2	US-09-972-484-2	Sequence 2, Appli	654	51.5	11.2	123	2	US-08-485-388-19	Sequence 19, Appl
582	52.5	11.4	1452	5	PCT-US93-04384-18	Sequence 18, Appl	655	51.5	11.2	123	2	US-08-478-853-19	Sequence 19, Appl
583	52.5	11.4	1452	5	PCT-US93-04692-2	Sequence 2, Appli	656	51.5	11.2	123	2	US-09-166-205B-19	Sequence 19, Appl
584	52.5	11.4	1453	1	US-08-308-872B-6	Sequence 6, Appli	657	51.5	11.2	123	5	PCT-US94-02629-19	Sequence 19, Appl
585	52.5	11.4	2000	3	US-09-502-698-82	Sequence 82, Appl	658	51.5	11.2	134	2	US-09-605-703B-1756	Sequence 1756, Ap
586	52.5	11.4	2037	2	US-09-306-998-3	Sequence 3, Appli	659	51.5	11.2	185	2	US-09-252-991A-20175	Sequence 20175, A
587	52.5	11.4	2046	2	US-09-949-016-9365	Sequence 9365, Ap	660	51.5	11.2	187	2	US-09-949-016-9179	Sequence 9179, Ap
588	52.5	11.4	2070	3	US-09-502-698-83	Sequence 83, Appl	661	51.5	11.2	211	2	US-09-130-491-4	Sequence 4, Appli
589	52	11.3	87	2	US-09-252-991A-17552	Sequence 17552, A	662	51.5	11.2	211	2	US-09-603-552-12	Sequence 12, Appl
590	52	11.3	105	2	US-09-288-143-209	Sequence 209, App	663	51.5	11.2	211	2	US-09-886-683A-4	Sequence 4, Appli
591	52	11.3	105	3	US-08-984-429-209	Sequence 209, App	664	51.5	11.2	211	2	US-09-949-016-6992	Sequence 6992, Ap
592	52	11.3	127	2	US-09-328-352-4209	Sequence 4209, App	665	51.5	11.2	211	2	US-09-999-833A-270	Sequence 270, App
593	52	11.3	132	2	US-09-454-279-6	Sequence 6, Appli	666	51.5	11.2	211	2	US-10-020-445A-270	Sequence 270, App
594	52	11.3	136	2	US-09-270-767-39814	Sequence 39814, A	667	51.5	11.2	211	2	US-09-978-189-270	Sequence 270, App
595	52	11.3	136	2	US-09-270-767-55031	Sequence 55031, A	668	51.5	11.2	211	2	US-10-017-085A-270	Sequence 270, App
596	52	11.3	160	2	US-09-583-110-5206	Sequence 5206, Ap	669	51.5	11.2	211	3	US-10-145-129A-270	Sequence 270, App
597	52	11.3	175	2	US-09-107-433-3565	Sequence 3565, Ap	670	51.5	11.2	211	3	US-10-013-929A-270	Sequence 270, App
598	52	11.3	175	2	US-09-270-767-46710	Sequence 46710, A	671	51.5	11.2	211	3	US-10-013-917A-270	Sequence 270, App
599	52	11.3	216	2	US-09-107-532A-3711	Sequence 3711, Ap	672	51.5	11.2	211	3	US-10-013-917A-270	Sequence 270, App
600	52	11.3	218	2	US-10-094-749-2232	Sequence 2232, Ap	673	51.5	11.2	212	1	US-08-461-853-35	Sequence 35, Appl
601	52	11.3	231	2	US-09-303-518D-432	Sequence 432, App	674	51.5	11.2	212	2	US-09-917-254-62	Sequence 62, Appl
602	52	11.3	260	2	US-09-025-059-3	Sequence 3, Appli	675	51.5	11.2	224	2	US-08-871-572B-13	Sequence 13, Appl
603	52	11.3	260	2	US-08-888-429A-26	Sequence 26, Appl	676	51.5	11.2	240	2	US-09-252-991A-30410	Sequence 30410, A
604	52	11.3	260	2	US-09-593-653-26	Sequence 26, Appl	677	51.5	11.2	241	2	US-10-076-069-4	Sequence 4, Appli
605	52	11.3	260	2	US-09-618-259-8	Sequence 8, Appli	678	51.5	11.2	247	2	US-09-949-016-11579	Sequence 11579, A
606	52	11.3	260	3	US-08-915-659A-10	Sequence 10, Appl	679	51.5	11.2	250	2	US-09-167-717-1	Sequence 1, Appli
607	52	11.3	261	2	US-09-454-279-16	Sequence 16, Appl	680	51.5	11.2	268	2	US-09-818-780-17	Sequence 17, Appl
608	52	11.3	262	2	US-09-303-518D-434	Sequence 434, App	681	51.5	11.2	268	2	US-09-818-780-94	Sequence 94, Appl
609	52	11.3	267	2	US-09-248-796A-17580	Sequence 17580, A	682	51.5	11.2	292	2	US-09-205-258-1116	Sequence 1116, Ap
610	52	11.3	285	3	US-09-721-047A-21	Sequence 21, Appl	683	51.5	11.2	292	2	US-10-004-860-1116	Sequence 1116, Ap

392	54	11.7	447	5	PCT-US94-07280-20	Sequence 20, Appl	465	53	11.5	377	2	US-09-538-032-1199	Sequence 1199, Ap
393	54	11.7	447	5	PCT-US95-01087-20	Sequence 20, Appl	466	53	11.5	407	2	US-03-489-039A-13350	Sequence 13350, A
394	54	11.7	453	1	US-08-188-281B-16	Sequence 16, Appl	467	53	11.5	415	2	US-10-094-749-2139	Sequence 2139, Ap
395	54	11.7	453	1	PCT-US94-07280-16	Sequence 16, Appl	468	53	11.5	454	2	US-09-949-016-10198	Sequence 10198, A
396	54	11.7	453	5	PCT-US95-01087-16	Sequence 16, Appl	469	53	11.5	460	2	US-09-489-039A-13505	Sequence 13505, A
397	54	11.7	478	2	US-09-489-039A-7367	Sequence 7367, Ap	470	53	11.5	469	2	US-09-902-540-12213	Sequence 12213, A
398	54	11.7	490	1	US-08-188-281B-15	Sequence 15, Appl	471	53	11.5	473	2	US-10-094-749-1936	Sequence 1936, Ap
399	54	11.7	490	5	PCT-US94-07280-15	Sequence 15, Appl	472	53	11.5	474	2	US-09-489-039A-10791	Sequence 10791, A
400	54	11.7	490	5	PCT-US95-01087-15	Sequence 15, Appl	473	53	11.5	476	2	US-09-489-039A-12217	Sequence 12217, A
401	54	11.7	493	2	US-09-170-984-2	Sequence 2, Appl	474	53	11.5	482	2	US-09-438-185A-356	Sequence 356, App
402	54	11.7	518	2	US-09-540-236-3648	Sequence 3648, Ap	475	53	11.5	524	2	US-09-549-519-27	Sequence 27, Appl
403	54	11.7	880	2	US-09-538-092-601	Sequence 601, App	476	53	11.5	524	2	US-09-549-519-28	Sequence 28, Appl
404	54	11.7	891	2	US-09-252-991A-28689	Sequence 28689, A	477	53	11.5	563	2	US-09-949-016-8277	Sequence 8277, Ap
405	54	11.7	1036	2	US-09-902-540-14218	Sequence 14218, A	478	53	11.5	574	2	US-09-248-796A-16849	Sequence 16849, A
406	54	11.7	3623	2	US-09-341-461-2	Sequence 2, Appl	479	53	11.5	580	2	US-09-489-039A-8096	Sequence 8096, Ap
407	53.5	11.6	72	2	US-09-188-930-182	Sequence 182, App	480	53	11.5	605	2	US-09-902-540-12393	Sequence 12393, A
408	53.5	11.6	221	2	US-09-464-535-22	Sequence 22, Appl	481	53	11.5	661	2	US-09-540-236-3743	Sequence 3743, Ap
409	53.5	11.6	239	3	US-09-936-271C-71	Sequence 71, Appl	482	53	11.5	678	2	US-09-252-991A-20202	Sequence 20202, A
410	53.5	11.6	244	1	US-08-361-395-1	Sequence 1, Appl	483	53	11.5	686	2	US-09-252-991A-19332	Sequence 19332, A
411	53.5	11.6	244	2	US-09-618-259-11	Sequence 11, Appl	484	53	11.5	792	2	US-09-995-587A-11	Sequence 11, Appl
412	53.5	11.6	244	3	US-09-936-271C-84	Sequence 84, Appl	485	53	11.5	896	2	US-09-585-858-17	Sequence 17, Appl
413	53.5	11.6	272	2	US-09-583-110-3866	Sequence 3866, Ap	486	53	11.5	896	2	US-10-270-878-17	Sequence 17, Appl
414	53.5	11.6	284	2	US-09-902-540-16417	Sequence 16417, A	487	53	11.5	1016	2	US-09-252-991A-18914	Sequence 18914, A
415	53.5	11.6	302	2	US-09-252-991A-21655	Sequence 21655, A	488	53	11.5	1070	2	US-09-961-403-3	Sequence 3, Appl
416	53.5	11.6	308	2	US-09-489-039A-14278	Sequence 14278, A	489	53	11.5	1146	2	US-09-824-734-2	Sequence 2, Appl
417	53.5	11.6	310	2	US-09-107-433-4601	Sequence 4601, Ap	490	53	11.5	1238	2	US-09-904-065-2	Sequence 2, Appl
418	53.5	11.6	325	2	US-09-949-016-7713	Sequence 7713, Ap	491	53	11.5	1238	2	US-09-904-065-14	Sequence 14, Appl
419	53.5	11.6	359	2	US-08-637-670-37	Sequence 37, Appl	492	53	11.5	1240	1	US-08-680-326-37	Sequence 37, Appl
420	53.5	11.6	382	2	US-09-489-039A-13696	Sequence 13696, A	493	53	11.5	1240	2	US-09-904-065-4	Sequence 4, Appl
421	53.5	11.6	407	2	US-09-710-279-1578	Sequence 1578, Ap	494	53	11.5	1240	2	US-09-904-065-15	Sequence 15, Appl
422	53.5	11.6	410	1	US-08-723-415B-10	Sequence 10, Appl	495	53	11.5	1326	2	US-09-949-016-6806	Sequence 6806, Ap
423	53.5	11.6	410	2	US-09-189-627A-10	Sequence 10, Appl	496	53	11.5	1339	2	US-09-949-016-10448	Sequence 10448, A
424	53.5	11.6	410	2	US-09-710-861-10	Sequence 10, Appl	497	53	11.5	1478	2	US-09-949-016-8315	Sequence 8315, Ap
425	53.5	11.6	415	2	US-09-949-016-8808	Sequence 8808, Ap	498	52.5	11.4	21	2	US-09-962-756-592	Sequence 592, App
426	53.5	11.6	437	2	US-09-350-841A-1591	Sequence 1591, Ap	499	52.5	11.4	71	2	US-09-369-247-79	Sequence 79, Appl
427	53.5	11.6	438	2	US-08-486-099-105	Sequence 105, App	500	52.5	11.4	71	2	US-10-062-548-79	Sequence 79, Appl
428	53.5	11.6	438	2	US-08-360-107A-115	Sequence 115, App	501	52.5	11.4	123	2	US-09-107-532A-4652	Sequence 4652, Ap
429	53.5	11.6	438	2	US-08-484-223B-105	Sequence 105, App	502	52.5	11.4	126	2	US-08-331-625A-9	Sequence 9, Appl
430	53.5	11.6	438	2	US-08-919-597-105	Sequence 105, App	503	52.5	11.4	126	2	US-09-494-151-9	Sequence 9, Appl
431	53.5	11.6	438	2	US-08-475-668A-105	Sequence 105, App	504	52.5	11.4	126	2	US-09-972-484-9	Sequence 9, Appl
432	53.5	11.6	438	2	US-08-485-551A-105	Sequence 105, App	505	52.5	11.4	158	2	US-09-464-535-8	Sequence 8, Appl
433	53.5	11.6	438	2	US-08-471-913A-105	Sequence 105, App	506	52.5	11.4	167	2	US-09-438-185A-132	Sequence 132, App
434	53.5	11.6	438	2	US-08-485-264A-105	Sequence 105, App	507	52.5	11.4	216	2	US-09-464-535-28	Sequence 28, Appl
435	53.5	11.6	438	2	US-08-474-349A-105	Sequence 105, App	508	52.5	11.4	236	2	US-09-270-767-44948	Sequence 44948, A
436	53.5	11.6	438	2	US-08-470-896-105	Sequence 105, App	509	52.5	11.4	251	2	US-08-331-625A-59	Sequence 59, Appl
437	53.5	11.6	438	2	US-08-485-546A-105	Sequence 105, App	510	52.5	11.4	251	2	US-09-494-151-59	Sequence 59, Appl
438	53.5	11.6	438	2	US-08-487-266A-105	Sequence 105, App	511	52.5	11.4	251	2	US-09-972-484-59	Sequence 59, Appl
439	53.5	11.6	438	2	US-08-484-741-105	Sequence 105, App	512	52.5	11.4	384	2	US-08-907-608-6	Sequence 6, Appl
440	53.5	11.6	440	2	US-09-134-001C-3286	Sequence 3286, Ap	513	52.5	11.4	384	2	US-09-354-231B-6	Sequence 6, Appl
441	53.5	11.6	495	2	US-09-275-252A-5	Sequence 5, Appl	514	52.5	11.4	384	2	US-09-354-231B-10	Sequence 10, Appl
442	53.5	11.6	550	1	US-08-279-700-16	Sequence 16, Appl	515	52.5	11.4	384	2	US-09-354-231B-12	Sequence 12, Appl
443	53.5	11.6	550	2	US-09-230-944-18	Sequence 18, Appl	516	52.5	11.4	384	2	US-09-133-962A-4	Sequence 4, Appl
444	53.5	11.6	550	2	US-09-230-944-20	Sequence 20, Appl	517	52.5	11.4	384	2	US-09-128-602B-6	Sequence 6, Appl
445	53.5	11.6	550	2	US-09-873-233A-18	Sequence 18, Appl	518	52.5	11.4	384	2	US-09-128-602B-8	Sequence 8, Appl
446	53.5	11.6	550	2	US-09-873-233A-20	Sequence 20, Appl	519	52.5	11.4	384	2	US-09-128-602B-10	Sequence 10, Appl
447	53.5	11.6	550	2	US-10-149-634-2	Sequence 2, Appl	520	52.5	11.4	384	2	US-09-128-602B-12	Sequence 12, Appl
448	53.5	11.6	898	2	US-10-449-315-11	Sequence 11, Appl	521	52.5	11.4	384	2	US-09-128-602B-12	Sequence 12, Appl
449	53	11.5	68	2	US-09-243-675-3	Sequence 3, Appl	522	52.5	11.4	384	2	US-09-482-887-6	Sequence 6, Appl
450	53	11.5	78	2	US-09-749-637A-228	Sequence 228, App	523	52.5	11.4	384	2	US-09-965-288-6	Sequence 6, Appl
451	53	11.5	165	2	US-10-104-047-2538	Sequence 2538, Ap	524	52.5	11.4	384	2	US-09-995-297-6	Sequence 6, Appl
452	53	11.5	223	2	US-09-605-703B-2326	Sequence 2326, Ap	525	52.5	11.4	384	2	US-09-995-297-8	Sequence 8, Appl
453	53	11.5	225	2	US-09-543-681A-4579	Sequence 4579, Ap	526	52.5	11.4	384	2	US-09-995-297-10	Sequence 10, Appl
454	53	11.5	237	3	US-09-936-271C-66	Sequence 66, Appl	527	52.5	11.4	384	2	US-09-995-297-12	Sequence 12, Appl
455	53	11.5	239	2	US-08-913-014A-2	Sequence 2, Appl	528	52.5	11.4	384	2	US-09-697-379-4	Sequence 4, Appl
456	53	11.5	251	3	US-09-653-285-2	Sequence 2, Appl	529	52.5	11.4	384	2	US-10-116-212A-4	Sequence 4, Appl
457	53	11.5	251	3	US-09-936-271C-67	Sequence 67, Appl	530	52.5	11.4	384	2	US-09-771-904A-6	Sequence 6, Appl
458	53	11.5	299	2	US-09-252-991A-24215	Sequence 24215, A	531	52.5	11.4	384	2	US-09-771-904A-8	Sequence 8, Appl
459	53	11.5	319	2	US-09-134-000C-6061	Sequence 6061, Ap	532	52.5	11.4	384	2	US-09-771-904A-10	Sequence 10, Appl
460	53	11.5	348	2	US-09-134-001C-4857	Sequence 4857, Ap	533	52.5	11.4	384	2	US-09-771-904A-12	Sequence 12, Appl
461	53	11.5	355	2	US-09-902-540-14706	Sequence 14706, A	534	52.5	11.4	396	2	US-09-198-452A-147	Sequence 147, App
462	53	11.5	356	2	US-09-664-840-2	Sequence 2, Appl	535	52.5	11.4	410	1	US-08-723-415B-11	Sequence 11, Appl
463	53	11.5	377	1	US-08-188-277B-4	Sequence 4, Appl	536	52.5	11.4	410	1	US-08-428-131-2	Sequence 2, Appl
464	53	11.5	377	1	US-08-429-964-78	Sequence 78, Appl	537	52.5	11.4	410	1	US-08-602-846-2	Sequence 2, Appl

246	55.5	12.0	559	2	US-08-767-993-15	Sequence 15, Appl	319	54.5	11.8	631	2	US-09-328-352-6860	Sequence 6860, Ap
247	55.5	12.0	687	1	US-08-555-568B-21	Sequence 21, Appl	320	54.5	11.8	752	1	US-08-281-193-2	Sequence 2, Appl
248	55.5	12.0	687	2	US-09-519-223-21	Sequence 21, Appl	321	54.5	11.8	752	1	US-08-422-106-2	Sequence 2, Appl
249	55.5	12.0	687	2	US-09-927-180-21	Sequence 21, Appl	322	54.5	11.8	752	1	US-08-735-716-2	Sequence 2, Appl
250	55.5	12.0	688	1	US-08-555-568B-23	Sequence 23, Appl	323	54.5	11.8	752	1	US-08-555-568B-2	Sequence 2, Appl
251	55.5	12.0	688	2	US-09-519-223-23	Sequence 23, Appl	324	54.5	11.8	752	1	US-09-519-223-2	Sequence 2, Appl
252	55.5	12.0	688	2	US-09-927-180-23	Sequence 23, Appl	325	54.5	11.8	752	1	US-09-927-180-2	Sequence 2, Appl
253	55.5	12.0	688	2	US-09-949-016-10948	Sequence 10948, A	326	54.5	11.8	752	5	PCT-US95-08069-2	Sequence 2, Appl
254	55.5	12.0	887	2	US-09-077-940A-2	Sequence 2, Appl	327	54.5	11.8	765	2	US-09-949-016-7844	Sequence 7844, Ap
255	55.5	12.0	888	2	US-09-077-940A-4	Sequence 4, Appl	328	54.5	11.8	780	2	US-09-902-540-10063	Sequence 10063, A
256	55.5	12.0	888	2	US-10-036-041-35	Sequence 35, Appl	329	54.5	11.8	781	1	US-08-280-690-2	Sequence 2, Appl
257	55.5	12.0	968	2	US-09-228-986-76	Sequence 76, Appl	330	54.5	11.8	895	1	US-08-123-161A-8	Sequence 8, Appl
258	55.5	12.0	968	2	US-10-101-464A-76	Sequence 76, Appl	331	54.5	11.8	895	1	US-08-483-278-8	Sequence 8, Appl
259	55	11.9	124	2	US-09-270-767-33906	Sequence 33906, A	332	54.5	11.8	895	2	US-09-949-016-6490	Sequence 6490, Ap
260	55	11.9	124	2	US-09-270-767-49123	Sequence 49123, A	333	54.5	11.8	920	2	US-09-949-016-7178	Sequence 7178, Ap
261	55	11.9	205	2	US-09-248-796A-15224	Sequence 15224, A	334	54.5	11.8	1021	2	US-10-094-749-3055	Sequence 3055, Ap
262	55	11.9	232	1	US-08-456-670B-39	Sequence 39, Appl	335	54	11.7	135	1	US-08-188-281B-6	Sequence 6, Appl
263	55	11.9	232	1	US-09-372-036-39	Sequence 39, Appl	336	54	11.7	135	5	PCT-US94-07280-6	Sequence 6, Appl
264	55	11.9	359	2	US-09-248-796A-18202	Sequence 18202, A	337	54	11.7	135	5	PCT-US95-01087-6	Sequence 6, Appl
265	55	11.9	376	2	US-09-103-331-42	Sequence 42, Appl	338	54	11.7	172	1	US-08-188-281B-5	Sequence 5, Appl
266	55	11.9	376	2	US-09-631-594-51	Sequence 51, Appl	339	54	11.7	172	5	PCT-US94-07280-5	Sequence 5, Appl
267	55	11.9	381	2	US-09-248-796A-19630	Sequence 19630, A	340	54	11.7	172	5	PCT-US95-01087-5	Sequence 5, Appl
268	55	11.9	404	2	US-09-538-092-50	Sequence 50, Appl	341	54	11.7	178	2	US-09-936-588-42	Sequence 42, Appl
269	55	11.9	406	2	US-09-252-991A-20630	Sequence 20630, A	342	54	11.7	221	1	US-08-188-281B-2	Sequence 2, Appl
270	55	11.9	459	2	US-08-311-731A-47	Sequence 47, Appl	343	54	11.7	221	5	PCT-US94-07280-2	Sequence 2, Appl
271	55	11.9	478	1	US-08-456-670B-40	Sequence 40, Appl	344	54	11.7	221	5	PCT-US95-01087-2	Sequence 2, Appl
272	55	11.9	478	1	US-09-372-036-40	Sequence 40, Appl	345	54	11.7	241	2	US-09-005-298-46	Sequence 46, Appl
273	55	11.9	484	1	US-08-127-499A-26	Sequence 26, Appl	346	54	11.7	241	2	US-08-768-619-46	Sequence 46, Appl
274	55	11.9	484	1	US-08-482-847-26	Sequence 26, Appl	347	54	11.7	346	2	US-09-702-705-329	Sequence 329, App
275	55	11.9	512	1	US-08-173-508-4	Sequence 4, Appl	348	54	11.7	346	2	US-09-736-457-329	Sequence 329, App
276	55	11.9	512	1	US-08-265-310-4	Sequence 4, Appl	349	54	11.7	346	2	US-09-614-124B-329	Sequence 329, App
277	55	11.9	512	2	US-08-351-742-4	Sequence 4, Appl	350	54	11.7	346	2	US-09-671-325-329	Sequence 329, App
278	55	11.9	533	2	US-09-549-519-32	Sequence 32, Appl	351	54	11.7	346	2	US-09-589-184-329	Sequence 329, App
279	55	11.9	598	2	US-09-252-991A-25875	Sequence 25875, A	352	54	11.7	346	2	US-09-658-824-329	Sequence 329, App
280	55	11.9	666	1	US-08-083-590A-17	Sequence 17, Appl	353	54	11.7	346	2	US-10-017-754-329	Sequence 329, App
281	55	11.9	666	1	US-08-346-128-36	Sequence 36, Appl	354	54	11.7	346	2	US-09-519-642-329	Sequence 329, App
282	55	11.9	666	2	US-08-532-384-17	Sequence 17, Appl	355	54	11.7	346	2	US-09-519-642-329	Sequence 329, App
283	55	11.9	1481	1	US-08-616-844-40	Sequence 40, Appl	356	54	11.7	346	2	US-10-099-322-24	Sequence 24, Appl
284	55	11.9	1481	1	US-08-599-654-40	Sequence 40, Appl	357	54	11.7	346	2	US-10-099-322-96	Sequence 96, Appl
285	55	11.9	1481	2	US-08-944-868A-40	Sequence 40, Appl	358	54	11.7	346	2	US-10-099-322-97	Sequence 97, Appl
286	55	11.9	1481	2	US-08-944-423A-40	Sequence 40, Appl	359	54	11.7	346	2	US-10-044-564-24	Sequence 24, Appl
287	55	11.9	1481	2	US-08-944-496-40	Sequence 40, Appl	360	54	11.7	346	2	US-10-044-564-96	Sequence 96, Appl
288	54.5	11.8	102	2	US-09-540-236-2816	Sequence 2816, Ap	361	54	11.7	346	2	US-10-044-564-97	Sequence 97, Appl
289	54.5	11.8	139	2	US-09-270-767-32364	Sequence 32364, A	362	54	11.7	348	2	US-10-099-322-69	Sequence 69, Appl
290	54.5	11.8	139	2	US-09-270-767-47581	Sequence 47581, A	363	54	11.7	348	2	US-10-099-322-98	Sequence 98, Appl
291	54.5	11.8	221	2	US-09-270-767-31937	Sequence 31937, A	364	54	11.7	348	2	US-10-099-322-99	Sequence 99, Appl
292	54.5	11.8	221	2	US-09-270-767-47154	Sequence 47154, A	365	54	11.7	348	2	US-10-044-564-69	Sequence 69, Appl
293	54.5	11.8	240	2	US-09-902-540-11028	Sequence 11028, A	366	54	11.7	348	2	US-10-044-564-98	Sequence 98, Appl
294	54.5	11.8	241	2	US-08-925-811-59	Sequence 59, Appl	367	54	11.7	348	2	US-10-044-564-99	Sequence 99, Appl
295	54.5	11.8	287	2	US-09-634-238-278	Sequence 278, App	368	54	11.7	377	1	US-08-188-281B-17	Sequence 17, Appl
296	54.5	11.8	384	1	US-08-675-650B-4	Sequence 4, Appl	369	54	11.7	377	5	PCT-US94-07280-17	Sequence 17, Appl
297	54.5	11.8	384	1	US-08-675-650B-6	Sequence 6, Appl	370	54	11.7	377	5	PCT-US95-01087-17	Sequence 17, Appl
298	54.5	11.8	384	2	US-08-907-608-2	Sequence 2, Appl	371	54	11.7	395	2	US-09-540-236-2520	Sequence 2520, Ap
299	54.5	11.8	384	2	US-08-907-608-4	Sequence 4, Appl	372	54	11.7	397	1	US-08-188-281B-11	Sequence 11, Appl
300	54.5	11.8	384	2	US-09-059-769-10	Sequence 10, Appl	373	54	11.7	397	5	PCT-US94-07280-11	Sequence 11, Appl
301	54.5	11.8	384	2	US-09-354-231B-2	Sequence 2, Appl	374	54	11.7	397	5	PCT-US95-01087-11	Sequence 11, Appl
302	54.5	11.8	384	2	US-09-354-231B-4	Sequence 4, Appl	375	54	11.7	410	1	US-08-188-281B-18	Sequence 18, Appl
303	54.5	11.8	384	2	US-09-128-602B-2	Sequence 2, Appl	376	54	11.7	410	5	PCT-US94-07280-18	Sequence 18, Appl
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305	54.5	11.8	384	2	US-09-482-287-2	Sequence 2, Appl	378	54	11.7	412	1	US-09-489-039A-9118	Sequence 9118, Ap
306	54.5	11.8	384	2	US-09-482-287-4	Sequence 4, Appl	379	54	11.7	417	1	US-08-188-281B-19	Sequence 19, Appl
307	54.5	11.8	384	2	US-09-966-888-2	Sequence 2, Appl	380	54	11.7	417	5	PCT-US94-07280-19	Sequence 19, Appl
308	54.5	11.8	384	2	US-09-966-888-4	Sequence 4, Appl	381	54	11.7	417	5	PCT-US95-01087-19	Sequence 19, Appl
309	54.5	11.8	384	2	US-09-995-297-2	Sequence 2, Appl	382	54	11.7	434	1	US-08-188-281B-10	Sequence 10, Appl
310	54.5	11.8	384	2	US-09-995-297-4	Sequence 4, Appl	383	54	11.7	434	5	PCT-US94-07280-10	Sequence 10, Appl
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317	54.5	11.8	481	3	US-10-288-930-77	Sequence 77, Appl	390	54	11.7	443	2	US-10-115-123-147	Sequence 147, App
318	54.5	11.8	613	2	US-09-328-352-7962	Sequence 7962, Ap	391	54	11.7	447	1	US-08-188-281B-20	Sequence 20, Appl

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101	60	13.0	337	2	US-08-930-830B-2	Sequence 2, Appli	174	56.5	12.3	233	2	US-09-056-556-76	Sequence 76, Appl
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111	59	12.8	854	2	US-09-833-466-12	Sequence 12, Appl	184	56.5	12.3	419	2	US-08-115-753-33	Sequence 33, Appl
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118	58.5	12.7	260	2	US-09-999-833A-395	Sequence 395, App	191	56.5	12.3	757	2	US-09-949-016-7121	Sequence 7121, Ap
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124	58.5	12.7	260	3	US-10-013-929A-395	Sequence 395, App	197	56.5	12.3	852	2	US-08-473-089-67	Sequence 67, Appl
125	58.5	12.7	260	3	US-09-936-271C-83	Sequence 83, Appl	198	56.5	12.3	852	2	US-08-487-072A-59	Sequence 59, Appl
126	58.5	12.7	260	3	US-10-013-917A-395	Sequence 395, App	199	56.5	12.3	852	2	US-08-487-072A-67	Sequence 67, Appl
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152	57.5	12.5	528	1	US-08-527-152-2	Sequence 2, Appli	225	55.5	12.0	262	1	US-08-767-993-2	Sequence 2, Appli
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154	57.5	12.5	1107	2	US-09-489-039A-8890	Sequence 8890, Ap	227	55.5	12.0	292	2	US-09-519-223-19	Sequence 19, Appl
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158	56.5	12.3	89	1	US-07-966-187-5	Sequence 5, Appli	231	55.5	12.0	384	1	US-09-354-231B-14	Sequence 14, Appl
159	56.5	12.3	89	1	US-08-371-121-4	Sequence 4, Appli	232	55.5	12.0	384	2	US-09-354-231B-16	Sequence 16, Appl
160	56.5	12.3	89	1	US-07-927-391-6	Sequence 6, Appli	233	55.5	12.0	384	2	US-09-354-231B-18	Sequence 18, Appl
161	56.5	12.3	89	2	US-08-115-753-15	Sequence 15, Appl	234	55.5	12.0	384	2	US-09-128-602B-14	Sequence 14, Appl
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163	56.5	12.3	168	2	US-09-898-659-16	Sequence 16, Appl	236	55.5	12.0	384	2	US-09-128-602B-18	Sequence 18, Appl
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167	56.5	12.3	205	2	US-09-072-596-81	Sequence 81, Appl	240	55.5	12.0	384	2	US-09-771-904A-14	Sequence 14, Appl
168	56.5	12.3	205	2	US-09-072-967-80	Sequence 80, Appl	241	55.5	12.0	384	2	US-09-771-904A-16	Sequence 16, Appl
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SUMMARIES

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74	66.5	14.4	552	2	US-09-949-016-8164 Sequence 8164, Ap
75	65.5	14.2	546	2	US-10-094-749-1953 Sequence 1953, Ap
76	64.5	14.0	729	2	US-09-248-796A-17121 Sequence 17121, A
77	63	13.7	627	2	US-10-222-100-3 Sequence 3, Appli
78	62.5	13.6	339	2	US-09-690-454-66 Sequence 66, Appl
79	62.5	13.6	339	2	US-10-036-041-80 Sequence 80, Appl
80	62.5	13.6	339	3	US-10-062-831-66 Sequence 66, Appl
81	62.5	13.6	340	3	US-09-690-454-174 Sequence 174, App
82	62.5	13.6	340	3	US-10-062-831-174 Sequence 174, App
83	62.5	13.6	389	2	US-09-328-352-7324 Sequence 7324, Ap
84	62	13.4	78	2	US-09-749-637A-342 Sequence 342, App
85	62	13.4	360	2	US-09-489-039A-8000 Sequence 8000, Ap
86	62	13.4	601	2	US-09-336-643A-4 Sequence 4, Appli
87	62	13.4	638	2	US-10-154-419-61 Sequence 3725, Ap
88	61.5	13.3	103	2	US-09-107-532A-3725 Sequence 925, App
89	61.5	13.3	433	2	US-09-198-452A-525 Sequence 860, App
90	61.5	13.3	453	2	US-09-438-185A-860 Sequence 3, Appli
91	61.5	13.3	549	2	US-09-120-365-3 Sequence 3, Appli
92	61.5	13.3	549	2	US-09-515-039-3 Sequence 41830, A
93	61.5	13.3	606	2	US-09-270-767-41830 Sequence 7, Appli
94	61.5	13.3	990	2	US-10-363-937-7 Sequence 12762, A
95	61	13.2	457	2	US-09-489-038A-12762 Sequence 341, App
96	60.5	13.1	106	2	US-09-149-476-341 Sequence 13, Appl
97	60.5	13.1	288	2	US-09-386-642-13 Sequence 83, Appl
98	60.5	13.1	638	2	US-10-154-419-83 Sequence 28424, A
99	60.5	13.1	998	2	US-09-252-991A-28424 Sequence 28424, A

Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1498
ID ADF74108 standard; protein; 178 AA.
DE Human cell adhesion inhibitor protein disadherin.
PN JP2003174885-A.
PD 24-JUN-2003.
PA (KOKU-) KOKURITSU GAN CENT SOCHO.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1499
ID ADG12707 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1500
ID ADH09367 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;

PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1489
ID ADB86285 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1490
ID ABM32316 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1491
ID ABM32621 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1492
ID ABM31706 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1493
ID ABM31096 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1494
ID ADD06015 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1495
ID ADG03010 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1496
ID ADG01717 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1497
ID ADF95892 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1480
ID ABO36977 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1481
ID ABO37587 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1482
ID ABM75377 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1483
ID ABM33657 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1484
ID ABO46412 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1485
ID ADA82977 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1486
ID ADB91706 standard; protein; 178 AA.
DE Human secreted protein #SEQ ID 652.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1487
ID AEM32011 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1488
ID ABM31401 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068762-A1.
PD 10-APR-2003.

PN US2003068681-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1461
ID ABM74767 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1462
ID ABM33962 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1463
ID ABM20421 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1464
ID ABO48913 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1465
ID ABR72978 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036122-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1466
ID ABO15620 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1467
ID ABR85335 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040065-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1468
ID ABO15315 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003044919-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1469
ID ABO17450 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003040077-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1470
ID ABO41247 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.

ID ABM17739 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1471
ID ABR85640 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1472
ID ABM77206 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1473
ID ABO28385 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1474
ID ABM23166 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1475
ID ABM30486 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1476
ID ABM21946 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1477
ID ABM21641 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1478
ID ABM15172 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 94; DB 7; Length 178;
Pred. No. 0.0035;
RESULT 1479
ID ABO41247 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.

PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1442
ID ABM05987 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1443
ID ABO39112 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1444
ID ABM34877 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1445
ID ABO51353 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1446
ID ABO04179 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1447
ID ABO10649 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1448
ID ABR77892 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1449
ID ABR79102 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1450
ID ABO24196 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1451
ID ABO40332 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1452
ID ABM02003 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1453
ID ABM78426 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1454
ID ABR90215 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1455
ID ABM27741 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1456
ID ABM13342 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1457
ID ABO32045 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1458
ID ABM14257 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1459
ID ABM08462 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1460
ID ABO40332 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.

PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1423
ID ABM19201 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1424
ID ABM19506 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1425
ID ABO46717 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1426
ID ABO49218 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1427
ID ABR69261 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1428
ID ABR89300 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1429
ID ABR72673 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1430
ID ABR74503 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1431
ID ABO18771 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1432
ID ABR80477 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1433
ID ABM01698 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1434
ID ABM02308 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1435
ID ABR87470 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1436
ID ABM13037 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1437
ID ABM30791 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1438
ID ABM24691 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1439
ID ABO29605 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1440
ID ABO31435 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1441
ID ABM14562 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1404
ID ABO40027 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1405
ID ABO50133 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1406
ID ABO51048 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1407
ID ABO05504 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1408
ID ABR74808 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1409
ID ABR77287 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1410
ID ABM18044 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1411
ID ABR96095 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1412
ID ABO22028 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1413
ID ABO20198 standard; protein; 178 AA.

DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1414
ID ABO24501 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1415
ID ABR86250 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1416
ID ABM10902 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1417
ID ABM76901 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1418
ID ABR89605 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1419
ID ABM12732 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1420
ID ABM06022 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1421
ID ABO35147 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 7; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1422
ID ABM03223 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068764-A1.
PD 10-APR-2003.

ID ABO30825 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1386
ID ABO31130 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1387
ID ABO27436 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1388
ID ABO30181 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1389
ID ABO05717 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1390
ID ABO15782 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1391
ID ABO08767 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1392
ID ABO42467 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1393
ID ABO38197 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1394
ID ABO46107 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068763-A1.

DE Human PRO polypeptide #271.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1395
ID ABO66910 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1396
ID ABO20654 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1397
ID ABO19811 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1398
ID ABO49523 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1399
ID ABO49828 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1400
ID ADA78906 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1401
ID ABO388385 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1402
ID ABO27131 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1403
ID ABO03528 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068763-A1.

Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1366
ID ABO47022 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1367
ID ABO47327 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1368
ID ADA83611 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1369
ID ABR71758 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1370
ID ABR72368 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1371
ID ABR98707 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1372
ID ABO07077 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1373
ID ABR85030 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1374
ID ABR73588 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1375
ID ABR76682 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044493-A1.

PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1376
ID ABR73283 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1377
ID ABM18349 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1378
ID ABO20808 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1379
ID ABO25551 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1380
ID ABO25856 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1381
ID ABR94265 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1382
ID ABR80172 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1383
ID ABM11512 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1384
ID ABO33119 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1385

Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1347
ID ABO51658 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1348
ID ABO51963 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1349
ID ABO50743 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1350
ID ABR79867 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1351
ID ABM17129 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1352
ID ABO18161 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1353
ID ABO21113 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1354
ID ABR97072 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1355
ID ABM12427 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1356
ID ABM16519 standard; protein; 178 AA.

DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1357
ID ABM24386 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1358
ID ABM14867 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1359
ID ABM04748 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1360
ID ABM06937 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1361
ID ABM09377 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1362
ID ABO39417 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1363
ID ABM75682 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1364
ID ABM25606 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1365
ID ABM20116 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

RESULT 1328
ID ABO22893 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1329
ID ABO23198 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1330
ID ABR92740 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1331
ID ABR81697 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1332
ID ABR78121 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1333
ID ABR89910 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1334
ID ABR26826 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1335
ID ABR13952 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1336
ID ABO28690 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1337
ID ABO30520 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064464-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1338
ID ABO07547 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1339
ID ABO04138 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1340
ID ABO37282 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1341
ID ABO41857 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1342
ID ABO35452 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1343
ID ABO25301 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1344
ID ABO47693 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1345
ID ABO47998 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1346
ID ABO48608 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 1309
ID ABM34267 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1310
ID ABM34572 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1311
ID ABO20503 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1312
ID ABO21418 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1313
ID ABO22333 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1314
ID ABR96767 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1315
ID ABR85945 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1316
ID ABR9927 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1317
ID ABM00783 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1318
ID ABM00478 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1319
ID ABO29910 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1320
ID ABM23776 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1321
ID ABM29571 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1322
ID ABO38502 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1323
ID ABO45802 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1324
ID ABM20726 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1325
ID ADA81813 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1326
ID ABO16840 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1327
ID ABO18466 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US200304920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;

RESULT 1290
ID ABM33047 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1291
ID ABM22861 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1292
ID ABM75072 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003096333-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1293
ID ADA80086 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1294
ID ABR96462 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1295
ID ABM02613 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1296
ID ABR86555 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1297
ID ABR86860 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1298
ID ABR16824 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1299
ID ABM29876 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1300
ID ABO29300 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1301
ID ABM24081 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1302
ID ABM23471 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1303
ID ABM22251 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1304
ID ABO37892 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1305
ID ABM28656 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1306
ID ABM28961 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1307
ID ABM66605 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1308
ID ABM75987 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;

DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1272
ID ABO40942 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1273
ID ABM35589 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1274
ID ABM33352 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1275
ID ABO52878 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1276
ID ABO50438 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1277
ID ABU99432 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1278
ID ABO04484 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1279
ID ABM18654 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1280
ID ABR97682 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1281
ID ABR80782 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1282
ID ABM01393 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1283
ID ABR88995 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1284
ID ABM13647 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1285
ID ABM21031 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1286
ID ABO42162 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1287
ID ABO42772 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1288
ID ABM10292 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1289
ID ABO38807 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;

ID	ABR97377 standard; protein; 178 AA.	
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.	
PN	US2003054491-A1.	
PD	20-MAR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	20.4%; Score 94; DB 6; Length 178;	
Best Local Similarity	43.9%; Pred. No. 0.0035;	
RESULT 1263		
ID	ABR87165 standard; protein; 178 AA.	
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.	
PN	US2003049778-A1.	
PD	13-MAR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	20.4%; Score 94; DB 6; Length 178;	
Best Local Similarity	43.9%; Pred. No. 0.0035;	
RESULT 1264		
ID	ABM11207 standard; protein; 178 AA.	
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.	
PN	US2003049782-A1.	
PD	13-MAR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	20.4%; Score 94; DB 6; Length 178;	
Best Local Similarity	43.9%; Pred. No. 0.0035;	
RESULT 1265		
ID	ABM28351 standard; protein; 178 AA.	
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.	
PN	US2003054476-A1.	
PD	20-MAR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	20.4%; Score 94; DB 6; Length 178;	
Best Local Similarity	43.9%; Pred. No. 0.0035;	
RESULT 1266		
ID	ABO32350 standard; protein; 178 AA.	
DE	Human secreted/transmembrane protein (PRO) #271.	
PN	US2003068733-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	20.4%; Score 94; DB 6; Length 178;	
Best Local Similarity	43.9%; Pred. No. 0.0035;	
RESULT 1267		
ID	ABM15477 standard; protein; 178 AA.	
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.	
PN	US2003068692-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	20.4%; Score 94; DB 6; Length 178;	
Best Local Similarity	43.9%; Pred. No. 0.0035;	
RESULT 1268		
ID	ABM06632 standard; protein; 178 AA.	
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.	
PN	US2003068709-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	20.4%; Score 94; DB 6; Length 178;	
Best Local Similarity	43.9%; Pred. No. 0.0035;	
RESULT 1269		
ID	ABM04443 standard; protein; 178 AA.	
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.	
PN	US2003068716-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	20.4%; Score 94; DB 6; Length 178;	
Best Local Similarity	43.9%; Pred. No. 0.0035;	
RESULT 1270		
ID	ABM22556 standard; protein; 178 AA.	
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.	
PN	US2003068740-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	20.4%; Score 94; DB 6; Length 178;	
Best Local Similarity	43.9%; Pred. No. 0.0035;	
RESULT 1271		
ID	ABM07852 standard; protein; 178 AA.	
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.	
PN	US2003068740-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	20.4%; Score 94; DB 6; Length 178;	
Best Local Similarity	43.9%; Pred. No. 0.0035;	
RESULT 1271		
ID	ABM07852 standard; protein; 178 AA.	
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.	
PN	US2003068740-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	20.4%; Score 94; DB 6; Length 178;	
Best Local Similarity	43.9%; Pred. No. 0.0035;	
RESULT 1271		
ID	ABM07852 standard; protein; 178 AA.	
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.	
PN	US2003068740-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	20.4%; Score 94; DB 6; Length 178;	
Best Local Similarity	43.9%; Pred. No. 0.0035;	
RESULT 1271		
ID	ABM07852 standard; protein; 178 AA.	
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.	
PN	US2003068740-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	20.4%; Score 94; DB 6; Length 178;	
Best Local Similarity	43.9%; Pred. No. 0.0035;	
RESULT 1271		
ID	ABM07852 standard; protein; 178 AA.	
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.	
PN	US2003068740-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	20.4%; Score 94; DB 6; Length 178;	
Best Local Similarity	43.9%; Pred. No. 0.0035;	
RESULT 1271		
ID	ABM07852 standard; protein; 178 AA.	
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.	
PN	US2003068740-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	20.4%; Score 94; DB 6; Length 178;	
Best Local Similarity	43.9%; Pred. No. 0.0035;	
RESULT 1271		
ID	ABM07852 standard; protein; 178 AA.	
DE	Human secreted polypeptide PRO6241, SEQ ID NO:542.	
PN	US2003068740-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	20.4%; Score 94; DB 6; Length 178;	
Best Local Similarity	43.9%; Pred.	

PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1234
ID ABM76596 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1235
ID ABM76292 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1236
ID ABM25911 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1237
ID ABM26216 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1238
ID ABO03569 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US20030316127-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1239
ID ABO02654 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1240
ID ABR90825 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1241
ID ABR73893 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1242
ID ABO17145 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1243
ID ABR94570 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044917-A1.

PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1244
ID ABR76077 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1245
ID ABR71453 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1246
ID ABR93350 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1247
ID ABR93655 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1248
ID ABR88080 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1249
ID ABO28080 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1250
ID ABO30215 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1251
ID ABO33424 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1252
ID ABO05112 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1253
ID ABR94570 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044917-A1.

DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1216
ID ABM06327 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1217
ID ABM03833 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1218
ID ABM35284 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1219
ID ABM6521 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1220
ID ABO48303 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1221
ID ABR93045 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1222
ID ABO41552 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1223
ID ABM11817 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1224
ID ARM02918 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073184-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1225
ID ABM16214 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1226
ID ABO27775 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1227
ID ABM29266 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1228
ID ABM07242 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1229
ID ABM21336 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1230
ID ABM09682 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1231
ID ABO41552 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1232
ID ABO36367 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1233
ID ABO43896 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068732-A1.
PD 10-APR-2003.

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PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1206
ID ABO03264 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US20030306131-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1207
ID ABR90520 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1208
ID ABR95180 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US200304930-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1209
ID ABR95180 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US200304930-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1210
ID ABR95485 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1211
ID ABO21723 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1212
ID ABR97987 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1213
ID ABR87775 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1214
ID ABR77816 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1215
ID ABR28046 standard; protein; 178 AA.
PD 05-JUN-2003.

PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1197
ID ABM77511 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1198
ID ABO28995 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1199
ID ABO31740 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1200
ID ABO80157 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1201
ID ABO40637 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1202
ID ABO36062 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1203
ID ABO44201 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1204
ID ADA78294 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1205
ID ABM24996 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003104539-A1.
PD 05-JUN-2003.
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Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1177
ID ABR70843 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1178
ID ABO05194 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1179
ID ABR69928 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032122-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1180
ID ABO0305 standard; protein; 178 AA.
DE Human PRO protein #271.
PN US2003036139-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1181
ID ABO93574 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003017541-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1182
ID ABO10127 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003017543-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1183
ID ABO09212 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036152-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1184
ID ABO10780 standard; protein; 178 AA.
DE Human secreted/transmembrane protein #271.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1185
ID ABO95789 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032115-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1186
ID ABO96998 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032140-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1187
ID ABR88690 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068743-A1.

RESULT 1187
ID ABR70843 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1188
ID ABO05194 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1189
ID ABO08602 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1190
ID ABO05809 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1191
ID ABR74198 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1192
ID ABR95790 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1193
ID ABR81087 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1194
ID ABR81392 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1195
ID ABO1088 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1196
ID ABR88690 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003068743-A1.

ID ABR66712 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1157
ID ABR91130 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1158
ID ABU94557 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1159
ID ABU79439 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1160
ID ABU86768 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1161
ID ABU87073 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1162
ID ABU94862 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1163
ID ABO04789 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1164
ID ABR70538 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1165
ID ABU98703 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1166
ID ABR66102 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.

PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1167
ID ABR64819 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1168
ID ABU79744 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1169
ID ABU93135 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1170
ID ABU96094 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1171
ID ABU91314 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1172
ID ABU90407 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1173
ID ABO09822 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1174
ID ABO11094 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1175
ID ABR71148 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1176
ID ABU87756 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003022293-A1.
PD 30-JAN-2003.

PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1136
ID ABU83113 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1137
ID ABU95169 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1138
ID ABU90717 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1139
ID ABU84228 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1140
ID ABU93879 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032119-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1141
ID ABR65124 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1142
ID ABR68956 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1143
ID ABO06772 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1144
ID ABR99317 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1145
ID ABU57201 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1146
ID ABU86153 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1147
ID ABU82440 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1148
ID ABU87451 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1149
ID ABU83923 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1150
ID ABO08297 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1151
ID ABU82008 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1152
ID ABU66172 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1153
ID ABR60001 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1154
ID ABU94189 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1155
ID ABO00062 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1156

ID ABU65839 standard; protein; 178 AA.
DE Human secreted/transmembrane protein, SEQ ID 542.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1116
ID AB007687 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1117
ID AB003874 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1118
ID ABR67322 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1119
ID AB015925 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1120
ID ABU56206 standard; protein; 178 AA.
DE Human secreted/transmembrane protein, PRO6241.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1121
ID ABU65534 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1122
ID ABU95479 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1123
ID ABU71382 standard; protein; 178 AA.
DE Human PRO6241 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1124
ID AB007992 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1125
ID ABR70233 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.

PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1126
ID ABR69566 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1127
ID AB001707 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1128
ID ABU81509 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1129
ID ABR60306 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1130
ID ABR68041 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1131
ID ABR65429 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1132
ID ABR68651 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1133
ID ABR72063 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1134
ID ABU85543 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1135
ID ABU89233 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.

Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1095
ID ABR99012 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1096
ID ABO16535 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1097
ID ABR92435 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1098
ID ABO19076 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1099
ID ABR78497 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1100
ID ABU85233 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1101
ID ABO00372 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1102
ID ABO11704 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1103
ID ABO02349 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1104
ID ADA41202 standard; protein; 178 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 20.4%; Score 94; DB 6; Length 178;

Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1105
ID ABU88923 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1106
ID ABU83618 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1107
ID ABO06419 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1108
ID ABR59455 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1109
ID ABO09517 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1110
ID ABO19381 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1111
ID ABO11399 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1112
ID ABR67017 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1113
ID ABO16230 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1114
ID ABO13936 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1115

PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1075
ID ABR65797 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1076
ID ABU9737 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1077
ID ABU82976 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1078
ID ABU90097 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1079
ID ABR68346 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1080
ID ABU96399 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1081
ID ABU92830 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1082
ID AB008907 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1083
ID AB002959 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1084
ID ABR75113 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;

Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1085
ID ABR94875 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1086
ID ABU85848 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1087
ID ABU99008 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1088
ID ABU98223 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1089
ID ABU91929 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1090
ID ABU89622 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1091
ID ABU86463 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1092
ID ABU67676 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1093
ID ABU80704 standard; protein; 178 AA.
DE Human PRO protein #271.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1094
ID ABR99622 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO:542.
PN US2003040063-A1.
PD 27-FEB-2003.

Best Local Similarity 40.0%; Pred. No. 3.1e-05;
RESULT 1056
ID ADH74323 standard; protein; 69 AA.
DE Human secreted protein #287.
PN US2003225248-A1.
PD 04-DEC-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.0%; Score 106; DB 8; Length 69;
Best Local Similarity 40.0%; Pred. No. 3.1e-05;
RESULT 1057
ID ABG26346 standard; protein; 110 AA.
DE Novel human diagnostic protein #26337.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.9%; Score 105.5; DB 4; Length 110;
Best Local Similarity 33.8%; Pred. No. 6.5e-05;
RESULT 1058
ID AAY13121 standard; protein; 72 AA.
DE Human secreted protein encoded by 5' EST SEQ ID NO: 135.
PN WO9906552-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 21.6%; Score 99.5; DB 2; Length 72;
Best Local Similarity 36.4%; Pred. No. 0.0022;
RESULT 1059
ID ABP03457 standard; protein; 63 AA.
DE Human ORFX protein sequence SEQ ID NO: 6896.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 20.8%; Score 96; DB 5; Length 63;
Best Local Similarity 32.8%; Pred. No. 0.00051;
RESULT 1060
ID ABG75825 standard; protein; 80 AA.
DE Transporters and ion channels protein 7, TRICH-7.
PN WO2003016493-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 20.6%; Score 95; DB 6; Length 80;
Best Local Similarity 31.3%; Pred. No. 0.00092;
RESULT 1061
ID ABM85184 standard; protein; 148 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO: 5433.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 20.6%; Score 95; DB 8; Length 148;
Best Local Similarity 36.5%; Pred. No. 0.002;
RESULT 1062
ID ABR82718 standard; protein; 115 AA.
DE Human IWU-1 protein.
PN WO2003064603-A2.
PD 07-AUG-2003.
PA (UTRP) UNIV ROCHESTER.
Query Match 20.4%; Score 94; DB 7; Length 115;
Best Local Similarity 43.9%; Pred. No. 0.002;
RESULT 1063
ID ABM85185 standard; protein; 147 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO: 5434.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 20.4%; Score 94; DB 8; Length 147;
Best Local Similarity 43.9%; Pred. No. 0.0027;
RESULT 1064
ID AAY13945 standard; protein; 178 AA.
DE Human transmembrane protein, HP10479.
PN WO9918203-A2.
PD 15-APR-1999.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match 20.4%; Score 94; DB 2; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1065
ID AAY41674 standard; protein; 178 AA.
DE Human channel-related molecule HCRM-2.
PN WO9943807-A2.
PD 02-SEP-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 20.4%; Score 94; DB 2; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1066
ID AAU29294 standard; protein; 178 AA.
DE Human PRO polypeptide sequence #271.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 20.4%; Score 94; DB 4; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1067
ID AAM38819 standard; protein; 178 AA.
DE Human polypeptide SEQ ID NO 1964.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 20.4%; Score 94; DB 4; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1068
ID ABB90357 standard; protein; 178 AA.
DE Human polypeptide SEQ ID NO 2733.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 20.4%; Score 94; DB 5; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1069
ID AAO17172 standard; protein; 178 AA.
DE Human secreted protein SEQ ID NO: 71.
PN WO200228877-A1.
PD 11-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 20.4%; Score 94; DB 5; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1070
ID ABG64783 standard; protein; 178 AA.
DE Human albumin fusion protein #1458.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 20.4%; Score 94; DB 5; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1071
ID ABUS8670 standard; protein; 178 AA.
DE Human PRO polypeptide #271.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1072
ID ABUS88218 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein PRO6241.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1073
ID ABUS84533 standard; protein; 178 AA.
DE Human secreted/transmembrane protein (PRO) #271.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 20.4%; Score 94; DB 6; Length 178;
Best Local Similarity 43.9%; Pred. No. 0.0035;
RESULT 1074
ID ABR66407 standard; protein; 178 AA.
DE Human secreted polypeptide PRO6241, SEQ ID NO: 542.

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Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1046
ID ADU03354 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1047
ID ADZ03405 standard; protein; 120 AA.
DE Human secreted/transmembrane PRO1056 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 9; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1048
ID AEA38462 standard; protein; 120 AA.
DE Human secreted/transmembrane protein, #118.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 9; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1049
ID AEB14151 standard; protein; 120 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 434.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFOUR L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 24.4%; Score 112.5; DB 9; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1050
ID AED86349 standard; protein; 120 AA.
DE Human PRO amino acid sequence, seq id 434.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 9; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1051
ID ABB80585 standard; protein; 95 AA.
DE Human sbg1015258PLM protein.
PN WO200222802-A1.
PD 21-MAR-2002.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PA (GLAX ) GLAXO GROUP LTD.
Query Match 24.3%; Score 112; DB 5; Length 95;
Best Local Similarity 35.9%; Pred. No. 8.1e-06;
RESULT 1052
ID AAW75005 standard; protein; 69 AA.
DE Human secreted protein encoded by gene 154 clone HB6FL83.
PN WO9839448-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.0%; Score 106; DB 7; Length 69;
Best Local Similarity 40.0%; Pred. No. 3.1e-05;
RESULT 1053
ID ABG95466 standard; protein; 69 AA.
DE Human novel secreted protein #287.
PN US6420526-B1.
PD 16-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.0%; Score 106; DB 5; Length 69;
Best Local Similarity 40.0%; Pred. No. 3.1e-05;
RESULT 1054
ID ABO34660 standard; protein; 69 AA.
DE Region of human secreted protein encoded by cDNA sequence #287.
PN US2003049618-A1.
PD 13-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFL/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 23.0%; Score 106; DB 6; Length 69;
Best Local Similarity 40.0%; Pred. No. 3.1e-05;
RESULT 1055
ID ADI23321 standard; protein; 69 AA.
DE Novel human secreted protein seq id 606.
PN US2003175858-A1.
PD 18-SEP-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFL/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 23.0%; Score 106; DB 7; Length 69;
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PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1028
ID ADH28614 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1029
ID ADG54759 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1030
ID ADG59799 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1031
ID ADI18223 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1032
ID ADG09966 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1033
ID ADI15437 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1034
ID ADG09314 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1035
ID ADI14769 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1036
ID ADI18364 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1037
ID ADJ63645 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1038
ID ADJ77540 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1039
ID ADJ65662 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1040
ID ADM27798 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1041
ID ADM42522 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1042
ID ADM28384 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1043
ID ADI95866 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1044
ID ADI96418 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1045
ID ADS32370 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
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ID ADG56967 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1010
ID ADG55863 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1011
ID ADG58623 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1012
ID ADG70989 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1013
ID ADG58071 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1014
ID ADG53655 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1015
ID ADG71541 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1016
ID ADG81728 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1017
ID ADH19445 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1018
ID ADH30690 standard; protein; 120 AA.
DE Human PRO polypeptide #217.

PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1019
ID ADH12057 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1020
ID ADG52479 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1021
ID ADG54207 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1022
ID ADG81176 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1023
ID ADG56415 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1024
ID ADH12681 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1025
ID ADH20938 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1026
ID ADG61527 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1027
ID ADH19978 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003219856-A1.
PD 27-NOV-2003.

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Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 991
ID ADG16820 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 992
ID ADG05279 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 993
ID ADG19546 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 994
ID ADG13383 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 995
ID ADG08440 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 996
ID ADG15610 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 997
ID ADF97008 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 998
ID ADG06193 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 999
ID ADG23777 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1000
ID ADG04066 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1001
ID ADG24967 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1002
ID ADG07264 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1003
ID ADG07816 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1004
ID ADG55311 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1005
ID ADG60975 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1006
ID ADG62079 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1007
ID ADG82280 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1008
ID ADG57519 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 1009
ID ADG57519 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
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PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 973
ID ADE94765 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 974
ID ADE91176 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 975
ID ADF35325 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 976
ID ADE95317 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 977
ID ADE93427 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 978
ID ADFJ5008 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 979
ID ADE92323 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 980
ID ADE90624 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 981
ID ADE91771 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 982
ID ADG11575 standard; protein; 120 AA.
DE Human PRO1056 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 983
ID ADG02350 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 984
ID ADG22136 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 985
ID ADG20206 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 986
ID ADF98112 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 987
ID ADG24329 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 988
ID ADF98683 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 989
ID ADG03514 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 990
ID ADF99235 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
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ID ADH99872 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 955
ID ADH81445 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 956
ID ADM82614 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 957
ID ADN16013 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 958
ID ADN16642 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 959
ID ADN15461 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 960
ID ADN14909 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 961
ID ADC81171 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 962
ID ADD76619 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 963
ID ADD87983 standard; protein; 120 AA.
DE Human PRO polypeptide #217.

PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 964
ID ADD86387 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 965
ID ADE75835 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 966
ID ADE23411 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 967
ID ADE23963 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 968
ID ADE24606 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 969
ID ADD87431 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 970
ID ADE89297 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 971
ID ADE18436 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 972
ID ADE88745 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199054-A1.

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Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 936
ID AD80624 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 937
ID AD80663 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 938
ID AD840947 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 939
ID ADE04746 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 940
ID ADE92875 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 941
ID ADF67126 standard; protein; 120 AA.
DE Human PRO1056 amino acid sequence SEQ ID NO:199.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 942
ID ADG21584 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 943
ID ADG23225 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 944
ID ADF97560 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 945
ID ADG80624 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 946
ID ADG80072 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 947
ID ADH53364 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 948
ID ADH55916 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 949
ID ADI33380 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 950
ID ADI64135 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 951
ID ADI65084 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 952
ID ADI63583 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 953
ID ADH81997 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 954
ID ADH81997 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 955
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PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 918
ID ADE22307 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 919
ID ADD79531 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 920
ID ADE42067 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 921
ID ADE17884 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 922
ID ADD92016 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 923
ID ADE33479 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 924
ID ADE34031 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 925
ID ADD80083 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 926
ID ADD93120 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194768-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 927
ID ADE19540 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 928
ID ADE18988 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 929
ID ADE43184 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 930
ID ADD95973 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 931
ID ADE22859 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 932
ID ADD78977 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 933
ID ADE26189 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 934
ID ADE32927 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 935
ID ADE42619 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 899
ID ADD06818 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 900
ID ADD09536 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 901
ID ADC83065 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 902
ID ADD41249 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 903
ID ADD52388 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 904
ID ADD53128 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 905
ID ADD53680 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 906
ID ADD55172 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 907
ID ADD56130 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 908

ID ADD51836 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 909
ID ADD02635 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 910
ID ADD02069 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 911
ID ADD54251 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 912
ID ADD54568 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 913
ID ADD92568 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 914
ID ADD91464 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 915
ID ADE04078 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 916
ID ADE26722 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 917
ID ADE32375 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.

Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 880
ID ADC59137 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 881
ID ADC56015 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 882
ID ADC38585 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 883
ID ADC14499 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 884
ID ADD08031 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003086623-A1.
PD 10-APR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 885
ID ADD03259 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 886
ID ADC90251 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 887
ID ADC81856 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 888
ID ADC69670 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194770-A1.
PD 16-OCT-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 889
ID ADC48559 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 890
ID ADD10088 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 891
ID ADD07498 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 892
ID ADD04663 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 893
ID ADC82389 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 894
ID ADC80619 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 895
ID ADD11126 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 896
ID ADC48007 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 897
ID ADD08569 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 898
ID ADC80067 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087358-A1.
PD 08-MAY-2003.

Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 861
ID ADB35103 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 862
ID ADB36207 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 863
ID ADB46602 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 864
ID ADC57679 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 865
ID ADC55043 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 866
ID ADC11910 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 867
ID ADC56332 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 868
ID ADC07387 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 869
ID ADC11377 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 870
ID ADC50475 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 871
ID ADC72022 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 872
ID ADC60001 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 873
ID ADC53008 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 874
ID ADC57362 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 875
ID ADC60553 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 876
ID ADC51028 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 877
ID ADC65555 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 878
ID ADC54653 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 879
ID ADC53614 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein Seq ID434.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

DE Human secreted/transmembrane protein PRO1056.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 843
ID ADA67055 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 844
ID ADB22916 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US200307711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 845
ID ADB23689 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 846
ID ADA92411 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 847
ID ADB15474 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 848
ID ADB38726 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 849
ID ADB96207 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 850
ID ADB38174 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 851
ID ADB66646 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 852
ID ADB89726 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 853
ID ADB90458 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 854
ID ADB39559 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 855
ID ADB47182 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 856
ID ADB86789 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 857
ID ADB77394 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 858
ID ADB34551 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 859
ID ADB35655 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 860
ID ADB33999 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

DE Human PRO polypeptide #217.
PN US2003082759-A1.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 824
ID ADB26327 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 825
ID ADB21812 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 826
ID ADA77591 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 827
ID ADB18331 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 828
ID ADA87014 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 829
ID ADA88117 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 830
ID ADA46505 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 831
ID ADB28535 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 832
ID ADB29087 standard; protein; 120 AA.
DE Human PRO polypeptide #217.

PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 833
ID ABO53155 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 834
ID ADA77039 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 835
ID ADA22322 standard; protein; 120 AA.
DE Human secreted/transmembrane polypeptide PRO1056.
PN US2003040473-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 836
ID ADA88669 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 837
ID ADA97674 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 838
ID ADB27431 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 839
ID ADB22364 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 840
ID ABO22525 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 841
ID ADA06488 standard; protein; 120 AA.
DE Human secreted/transmembrane PRO polypeptide #50.
PN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 7; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 842
ID ADA39181 standard; protein; 120 AA.

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Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 805
ID ADAB2317 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 806
ID ADA75280 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 807
ID ADA85358 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 808
ID ADA84806 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 809
ID ADB30062 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 810
ID ADA80590 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 811
ID ADA75832 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 812
ID ADA38640 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 813
ID ADA47057 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 814
ID ADB25353 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 815
ID ADA93529 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 816
ID ADB26879 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 817
ID ADB31166 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 818
ID ADA92761 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 819
ID ADA61094 standard; protein; 120 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 820
ID ADB24241 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 821
ID ADA96570 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 822
ID ADA81142 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 823
ID ADA96018 standard; protein; 120 AA.
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ID ADA67607 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 787
ID ADB30614 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 788
ID ADA85910 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 789
ID ADA1727 standard; protein; 120 AA.
DE Human PRO1056 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 790
ID ADA97122 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 791
ID ADA79426 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 792
ID ADA87565 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 793
ID ADB16767 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 794
ID ADA27835 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 795
ID ADA91859 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082694-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 796
ID ADB14922 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 797
ID ADB18883 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 798
ID ADA94098 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 799
ID ADB19994 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 800
ID ADB13306 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 801
ID ABO43365 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 802
ID ADA94415 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 803
ID ADA74560 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 804
ID ADB24793 standard; protein; 120 AA.
DE Human PRO polypeptide SEQ ID NO 434.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

DE Novel human secreted or transmembrane protein PRO826.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 768
ID ABU67062 standard; protein; 120 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 434.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 769
ID ABU92158 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 770
ID ABU10864 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 771
ID ABU81616 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 772
ID ABU88555 standard; protein; 120 AA.
DE Human secreted and transmembrane polypeptide PRO1056.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 773
ID ABO34069 standard; protein; 120 AA.
DE Human PRO1056 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 774
ID ADA45953 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 775
ID ADA76384 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 776
ID ADA19034 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 777
ID ADA61657 standard; protein; 120 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 778
ID ADB19442 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 779
ID ADB27983 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 780
ID ADA86462 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 781
ID ADB16026 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 782
ID ADA37710 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 783
ID ADA47812 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 784
ID ADA21396 standard; protein; 120 AA.
DE Human secreted/transmembrane polypeptide PRO1056.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 785
ID ADA10183 standard; protein; 120 AA.
DE Human secreted/transmembrane protein, PRO1056.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 786

PD 04-DEC-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 24.4%; Score 112.5; DB 8; Length 96;
Best Local Similarity 36.0%; Pred. No. 7.1e-06;
RESULT 749
ID AAY66680 standard; protein; 120 AA.
DE Membrane-bound protein PRO1056.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 3; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 750
ID AAU12388 standard; protein; 120 AA.
DE Human PRO1056 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 4; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 751
ID AAB65203 standard; protein; 120 AA.
DE Human PRO1056 (UNQ521) protein sequence SEQ ID NO:199.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 4; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 752
ID ABUS8018 standard; protein; 120 AA.
DE Human PRO polypeptide #50.
PN US2003027453-A1.
PD 06-FEB-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 753
ID ABUS9096 standard; protein; 120 AA.
DE Novel human secreted or transmembrane protein PRO1056.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 754
ID ABUS2608 standard; protein; 120 AA.
DE Human secreted/transmembrane protein PRO1056.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 755
ID ABO17832 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 756
ID ABUS60527 standard; protein; 120 AA.
DE Human secreted/transmembrane protein, #77.
PN US2002160394-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 757
ID ABUI3909 standard; protein; 120 AA.
DE Human PRO1056 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 758
ID ABUS1086 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 759
ID ABU72494 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 760
ID ABU66786 standard; protein; 120 AA.
DE Human PRO polypeptide #217.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 761
ID ABUS9867 standard; protein; 120 AA.
DE Novel secreted and transmembrane protein PRO1056.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 762
ID ABUS9243 standard; protein; 120 AA.
DE Human secreted/transmembrane protein, #77.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 763
ID ABO25940 standard; protein; 120 AA.
DE Human PRO1056 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 764
ID ABO25057 standard; protein; 120 AA.
DE Human secreted/transmembrane protein (PRO) #217.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 765
ID ABUS8949 standard; protein; 120 AA.
DE Human secreted/transmembrane protein, #77.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 766
ID ABU92327 standard; protein; 120 AA.
DE Novel human secreted and transmembrane protein PRO1056.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 24.4%; Score 112.5; DB 6; Length 120;
Best Local Similarity 36.0%; Pred. No. 9.4e-06;
RESULT 767
ID ABUS9392 standard; protein; 120 AA.

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PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC. 24.6%; Score 113.5; DB 4; Length 155;
Query Match 34.2%; Pred. No. 9.8e-06;
Best Local Similarity
RESULT 738
ID AAW51104 standard; protein; 95 AA.
DE A human phospholemman-like protein.
PN WO9814572-A1.
PD 09-APR-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 24.4%; Score 112.5; DB 2; Length 95;
Best Local Similarity 36.0%; Pred. No. 7e-06;
RESULT 739
ID AAU14575 standard; protein; 95 AA.
DE Human novel protein #446.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 24.4%; Score 112.5; DB 4; Length 95;
Best Local Similarity 36.0%; Pred. No. 7e-06;
RESULT 740
ID ABUS2798 standard; protein; 95 AA.
DE Human signal transduction-associated protein from DKF2phtb2_82117.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 24.4%; Score 112.5; DB 4; Length 95;
Best Local Similarity 36.0%; Pred. No. 7e-06;
RESULT 741
ID ADH80893 standard; protein; 95 AA.
DE Human polypeptide #210.
PN US2003232054-A1.
PD 18-DEC-2003.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.
PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOY/) CAO Y.
PA (DRMA/) DRMANAC R T.
Query Match 24.4%; Score 112.5; DB 8; Length 95;
Best Local Similarity 36.0%; Pred. No. 7e-06;
RESULT 742
ID ABM81305 standard; protein; 95 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82051, SEQ:3370.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 24.4%; Score 112.5; DB 8; Length 95;
Best Local Similarity 36.0%; Pred. No. 7e-06;
RESULT 743
ID ABE24249 standard; protein; 95 AA.
DE Novel human protein amino acid sequence - SEQ ID 918.
PN US2005266423-A1.
PD 01-DEC-2005.
PA (NUVE-) NUVELO INC.
Query Match 24.4%; Score 112.5; DB 10; Length 95;
Best Local Similarity 36.0%; Pred. No. 7e-06;
RESULT 744
ID AAW74882 standard; protein; 96 AA.
DE Human secreted protein encoded by gene 154 clone HE6FL83.
PN WO9839448-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 24.4%; Score 112.5; DB 2; Length 96;
Best Local Similarity 36.0%; Pred. No. 7.1e-06;
RESULT 745
ID ABG95333 standard; protein; 96 AA.
DE Human novel secreted protein #154.
PN US2003225248-A1.

PN US6420526-B1.
PD 16-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 24.4%; Score 112.5; DB 5; Length 96;
Best Local Similarity 36.0%; Pred. No. 7.1e-06;
RESULT 746
ID ABQ34527 standard; protein; 96 AA.
DE Region of human secreted protein encoded by cDNA sequence #154.
PN US2003049618-A1.
PD 13-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 24.4%; Score 112.5; DB 6; Length 96;
Best Local Similarity 36.0%; Pred. No. 7.1e-06;
RESULT 747
ID ADI23188 standard; protein; 96 AA.
DE Novel human secreted protein seq id 473.
PN US2003175858-A1.
PD 18-SEP-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 24.4%; Score 112.5; DB 7; Length 96;
Best Local Similarity 36.0%; Pred. No. 7.1e-06;
RESULT 748
ID ADH74190 standard; protein; 96 AA.
DE Human secreted protein #154.
PN US2003225248-A1.
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PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 28.0%; Score 129; DB 9; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.4e-08;
RESULT 725
ID AAW75106 standard; protein; 93 AA.
DE Human secreted protein encoded by gene 50 clone HHSDZ57.
PN WO9839446-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.0%; Score 129; DB 2; Length 93;
Best Local Similarity 41.3%; Pred. No. 5.5e-08;
RESULT 726
ID ABO01982 standard; protein; 93 AA.
DE Novel human secreted protein; 93 AA.
PN US2003027132-A1.
PD 06-FEB-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (FISC/) FISCHER C L.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D R.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN R.
PA (HUJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (SHIY/) SHI Y.
Query Match 28.0%; Score 129; DB 6; Length 93;
Best Local Similarity 41.3%; Pred. No. 5.5e-08;
RESULT 727
ID AD212383 standard; protein; 93 AA.
DE Human secreted protein sequence encoded by gene 50 SEQ ID NO:183.
PN US6878687-B1.
PD 12-APR-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.0%; Score 129; DB 9; Length 93;
Best Local Similarity 41.3%; Pred. No. 5.5e-08;
RESULT 728
ID ABO02067 standard; protein; 70 AA.
DE Novel human secreted protein associated protein fragment #12.
PN US2003027132-A1.
PD 06-FEB-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (FISC/) FISCHER C L.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D R.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN R.
PA (HUJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (SHIY/) SHI Y.

Query Match 26.2%; Score 121; DB 6; Length 70;
Best Local Similarity 44.9%; Pred. No. 3.9e-07;
RESULT 729
ID AD212469 standard; protein; 70 AA.
DE Human gene 50 secreted protein related sequence SEQ ID NO:269.
PN US6878687-B1.
PD 12-APR-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.2%; Score 121; DB 9; Length 70;
Best Local Similarity 44.9%; Pred. No. 3.9e-07;
RESULT 730
ID AAV12377 standard; protein; 63 AA.
DE Human 5' EST secreted protein SEQ ID NO:408.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST/) GENSET.
Query Match 24.7%; Score 114; DB 2; Length 63;
Best Local Similarity 43.1%; Pred. No. 2.7e-06;
RESULT 731
ID ADE58523 standard; protein; 92 AA.
DE Rat Protein O08589, SEQ ID NO 4398.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO/) GEN HOSPITAL CORP.
PA (FARB/) BAYER AG.
Query Match 24.7%; Score 114; DB 7; Length 92;
Best Local Similarity 31.6%; Pred. No. 4.3e-06;
RESULT 732
ID ADE58519 standard; protein; 92 AA.
DE Rat Protein O08589, SEQ ID NO 4394.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO/) GEN HOSPITAL CORP.
PA (FARB/) BAYER AG.
Query Match 24.7%; Score 114; DB 7; Length 92;
Best Local Similarity 31.6%; Pred. No. 4.3e-06;
RESULT 733
ID ADE83503 standard; protein; 92 AA.
DE Rat Protein O08589, SEQ ID NO 11099.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO/) GEN HOSPITAL CORP.
PA (FARB/) BAYER AG.
Query Match 24.7%; Score 114; DB 7; Length 92;
Best Local Similarity 31.6%; Pred. No. 4.3e-06;
RESULT 734
ID AAM38777 standard; protein; 138 AA.
DE Human polypeptide SEQ ID NO 1922.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 24.6%; Score 113.5; DB 4; Length 138;
Best Local Similarity 34.2%; Pred. No. 8.4e-06;
RESULT 735
ID AAU14339 standard; protein; 138 AA.
DE Human novel protein #210.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 24.6%; Score 113.5; DB 4; Length 138;
Best Local Similarity 34.2%; Pred. No. 8.4e-06;
RESULT 736
ID AEE23777 standard; protein; 138 AA.
DE Novel human protein amino acid sequence - SEQ ID 446.
PN US2005266423-A1.
PD 01-DEC-2005.
PA (NUVE-) NUVELO INC.
Query Match 24.6%; Score 113.5; DB 10; Length 138;
Best Local Similarity 34.2%; Pred. No. 8.4e-06;
RESULT 737
ID AAM40563 standard; protein; 155 AA.
DE Human polypeptide SEQ ID NO 5494.
PN WO200153312-A1.

PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.0%; Score 129; DB 2; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.4e-08;
RESULT 710
ID AAY24749 standard; protein; 92 AA.
DE Human phospholemmann homologue protein.
PN US5919655-A.
PD 06-JUL-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 28.0%; Score 129; DB 2; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.4e-08;
RESULT 711
ID AAY59689 standard; protein; 92 AA.
DE Secreted protein 26-44-1-B5-CL3_1.
PN WO9940189-A2.
PD 12-AUG-1999.
PA (GEST) GENSET.
Query Match 28.0%; Score 129; DB 2; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.4e-08;
RESULT 712
ID AAY48331 standard; protein; 92 AA.
DE Human prostate cancer-associated protein 28.
PN DE19811194-A1.
PD 16-SEP-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MEH.
Query Match 28.0%; Score 129; DB 2; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.4e-08;
RESULT 713
ID AAW92960 standard; protein; 92 AA.
DE Human PLM protein.
PN WO9905276-A1.
PD 04-FEB-1999.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 28.0%; Score 129; DB 2; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.4e-08;
RESULT 714
ID ABB97244 standard; protein; 92 AA.
DE Novel human protein SEQ ID NO: 512.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSQ INC.
Query Match 28.0%; Score 129; DB 5; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.4e-08;
RESULT 715
ID ABO02037 standard; protein; 92 AA.
DE Novel human secreted protein #105.
PN US2003027132-A1.
PD 06-FEB-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (FISC/) FISCHER C L.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D R.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R A.
PA (BREW/) BREWER L A.
PA (SHIY/) SHI Y.
Query Match 28.0%; Score 129; DB 6; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.4e-08;
RESULT 716
ID ADE58521 standard; protein; 92 AA.
DE Human Protein O00168, SEQ ID NO 4396.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 28.0%; Score 129; DB 7; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.4e-08;
RESULT 717
ID ADE58525 standard; protein; 92 AA.
DE Human Protein O00168, SEQ ID NO 4400.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 28.0%; Score 129; DB 7; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.4e-08;
RESULT 718
ID ADE83505 standard; protein; 92 AA.
DE Human Protein O00168, SEQ ID NO 11101.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 28.0%; Score 129; DB 7; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.4e-08;
RESULT 719
ID ADJ69464 standard; protein; 92 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1270.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 28.0%; Score 129; DB 7; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.4e-08;
RESULT 720
ID ADM77839 standard; protein; 92 AA.
DE Human protein #36.
PN US2003162176-A1.
PD 28-AUG-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLETT A.
PA (BOUG/) BOUGUELERET L.
Query Match 28.0%; Score 129; DB 7; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.4e-08;
RESULT 721
ID ADN05844 standard; protein; 92 AA.
DE Antipsoriatic protein sequence #1085.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 28.0%; Score 129; DB 8; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.4e-08;
RESULT 722
ID ADP19520 standard; protein; 92 AA.
DE Human secreted polypeptide #371.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 28.0%; Score 129; DB 8; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.4e-08;
RESULT 723
ID ADZ12438 standard; protein; 92 AA.
DE Human secreted protein sequence encoded by gene 50 SEQ ID NO:238.
PN US6878687-B1.
PD 12-APR-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.0%; Score 129; DB 9; Length 92;
Best Local Similarity 41.3%; Pred. No. 5.4e-08;
RESULT 724
ID ADZ89299 standard; protein; 92 AA.
DE Secreted protein encoded by extended EST cDNA #36.
PN US2005106599-A1.
PD 19-MAY-2005.

DE Novel human polypeptide NOV13b.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE/) ANDERSON D W.
PA (ZERH/) ZERHUSEN B D.
PA (LILL/) LI L.
PA (ZHON/) ZHONG M.
PA (CASM/) CASMAN S J.
PA (GERL/) GERLACH V.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (PENA/) PENA C E A.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (LEIT/) LEITE M W.
PA (MACT/) MACDOUGALL J R.
PA (TAUP/) TAUPIER R J.
PA (GUOX/) GUO X S.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (HJAL/) HJALT T.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (MALY/) MALYANKAR U M.
PA (PADI/) PADIGARU M.
PA (JIWW/) JI W.
PA (SMIT/) SMITHSON G.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (ELLE/) ELLERMAN K.
Query Match 46.5%; Score 214.5; DB 8; Length 116;
Best Local Similarity 54.5%; Pred. No. 1.1e-18;
RESULT 699
ID ABJ19333 standard; protein; 86 AA.
DE NOVX related protein SEQ ID NO 32.
PN WO200299082-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.4%; Score 209.5; DB 6; Length 86;
Best Local Similarity 54.0%; Pred. No. 3.1e-18;
RESULT 700
ID AD041666 standard; protein; 86 AA.
DE Novel human polypeptide NOV13a.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE/) ANDERSON D W.
PA (ZERH/) ZERHUSEN B D.
PA (LILL/) LI L.
PA (ZHON/) ZHONG M.
PA (CASM/) CASMAN S J.
PA (GERL/) GERLACH V.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (PENA/) PENA C E A.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (LEIT/) LEITE M W.
PA (MACT/) MACDOUGALL J R.
PA (TAUP/) TAUPIER R J.
PA (GUOX/) GUO X S.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (HJAL/) HJALT T.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (MALY/) MALYANKAR U M.
PA (PADI/) PADIGARU M.
PA (JIWW/) JI W.
PA (SMIT/) SMITHSON G.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (ELLE/) ELLERMAN K.
Query Match 45.4%; Score 209.5; DB 8; Length 111;
Best Local Similarity 41.2%; Pred. No. 8.8e-14;
RESULT 701
ID ABG75841 standard; protein; 67 AA.
DE Transporters and ion channels protein 23, TRICH-23.
PN WO2003016493-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 32.5%; Score 150; DB 6; Length 67;
Best Local Similarity 56.6%; Pred. No. 7.8e-11;
RESULT 708
ID ABU52799 standard; protein; 83 AA.
DE Human signal transduction-associated DKPzphfbr2_82i17 homologue.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 28.0%; Score 129; DB 4; Length 83;
Best Local Similarity 41.3%; Pred. No. 4.7e-08;
RESULT 709
ID AAW75161 standard; protein; 92 AA.
DE Human secreted protein encoded by gene 50 clone HHSD257.
PN WO9839446-A2.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (ELLE/) ELLERMAN K.
Query Match 45.4%; Score 209.5; DB 8; Length 86;
Best Local Similarity 54.0%; Pred. No. 3.1e-18;
RESULT 701
ID ABR47468 standard; protein; 113 AA.
DE Breast cancer associated protein sequence SEQ ID NO:168.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 41.5%; Score 191.5; DB 6; Length 113;
Best Local Similarity 42.1%; Pred. No. 8.4e-16;
RESULT 702
ID ADB75318 standard; protein; 113 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 41.5%; Score 191.5; DB 7; Length 113;
Best Local Similarity 42.1%; Pred. No. 8.4e-16;
RESULT 703
ID ADN40039 standard; protein; 113 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C409.
PN WO2003042561-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 41.5%; Score 191.5; DB 7; Length 113;
Best Local Similarity 42.1%; Pred. No. 8.4e-16;
RESULT 704
ID AAB53415 standard; protein; 150 AA.
DE Human colon cancer antigen protein sequence SEQ ID NO:955.
PN WO2000055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.5%; Score 191.5; DB 3; Length 150;
Best Local Similarity 42.1%; Pred. No. 1.2e-15;
RESULT 705
ID ADI36717 standard; protein; 111 AA.
DE Human PLML #1.
PN US2003225014-A1.
PD 04-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 38.1%; Score 175.5; DB 8; Length 111;
Best Local Similarity 41.2%; Pred. No. 8.8e-14;
RESULT 706
ID ADZ69595 standard; protein; 111 AA.
DE Human phospholeman-like protein (PLML) SEQ ID NO:3.
PN US2005101558-A1.
PD 12-MAY-2005.
PA (WART/) WAIT A T.
Query Match 38.1%; Score 175.5; DB 9; Length 111;
Best Local Similarity 41.2%; Pred. No. 8.8e-14;
RESULT 707
ID ABG75841 standard; protein; 67 AA.
DE Transporters and ion channels protein 23, TRICH-23.
PN WO2003016493-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 32.5%; Score 150; DB 6; Length 67;
Best Local Similarity 56.6%; Pred. No. 7.8e-11;
RESULT 708
ID ABU52799 standard; protein; 83 AA.
DE Human signal transduction-associated DKPzphfbr2_82i17 homologue.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 28.0%; Score 129; DB 4; Length 83;
Best Local Similarity 41.3%; Pred. No. 4.7e-08;
RESULT 709
ID AAW75161 standard; protein; 92 AA.
DE Human secreted protein encoded by gene 50 clone HHSD257.
PN WO9839446-A2.

DE Mouse Mat-8 polypeptide.
PN WO9605322-A1.
PD 22-FEB-1996.
PA (GEHO) GEN HOSPITAL CORP.
PA (HARD) HARVARD COLLEGE.
Query Match 52.4%; Score 214.5; DB 2; Length 88;
Best Local Similarity 57.8%; Pred. No. 2.8e-22;
RESULT 681
ID AAR90990 standard; protein; 87 AA.
DE Human Mat-8 polypeptide.
PN WO9605322-A1.
PD 22-FEB-1996.
PA (GEHO) GEN HOSPITAL CORP.
PA (HARD) HARVARD COLLEGE.
Query Match 46.5%; Score 214.5; DB 2; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.3e-19;
RESULT 682
ID AAY48304 standard; protein; 87 AA.
DE Human prostate cancer-associated protein 1.
PN DE19811194-A1.
PD 16-SEP-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 46.5%; Score 214.5; DB 2; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.3e-19;
RESULT 683
ID AAW92959 standard; protein; 87 AA.
DE Human MAT-8 protein.
PN WO9905276-A1.
PD 04-FEB-1999.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 46.5%; Score 214.5; DB 2; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.3e-19;
RESULT 684
ID AAM23962 standard; protein; 87 AA.
DE Human EST encoded protein SEQ ID NO: 1487.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 46.5%; Score 214.5; DB 4; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.3e-19;
RESULT 685
ID ABJ37036 standard; protein; 87 AA.
DE Human breast cancer / ovarian cancer related protein #12.
PN WO2003000012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 46.5%; Score 214.5; DB 6; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.3e-19;
RESULT 686
ID ABR47467 standard; protein; 87 AA.
DE Breast cancer associated protein sequence SEQ ID NO:166.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 46.5%; Score 214.5; DB 6; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.3e-19;
RESULT 687
ID ABP75985 standard; protein; 87 AA.
DE Human GENSET protein SEQ ID 192.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST) GENSET.
Query Match 46.5%; Score 214.5; DB 6; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.3e-19;
RESULT 688
ID ABP76150 standard; protein; 87 AA.
DE Human GENSET protein SEQ ID 476.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST) GENSET.
Query Match 46.5%; Score 214.5; DB 6; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.3e-19;
RESULT 689
ID ADO41668 standard; protein; 116 AA.
DE ADO41668 standard; protein; 116 AA.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 46.5%; Score 214.5; DB 7; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.3e-19;
RESULT 690
ID ADM40040 standard; protein; 87 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C410.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 46.5%; Score 214.5; DB 7; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.3e-19;
RESULT 691
ID ADI36718 standard; protein; 87 AA.
DE Human PLML #2.
PN US2003225014-A1.
PD 04-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 46.5%; Score 214.5; DB 8; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.3e-19;
RESULT 692
ID ADK70447 standard; protein; 87 AA.
DE Respiratory disease differentially expressed protein #13.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 46.5%; Score 214.5; DB 8; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.3e-19;
RESULT 693
ID ADQ80368 standard; protein; 87 AA.
DE FXD domain containing ion transport regulator 3 protein.
PN WO2004063709-A2.
PD 29-JUL-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 46.5%; Score 214.5; DB 8; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.3e-19;
RESULT 694
ID ADZ69596 standard; protein; 87 AA.
DE Human phospholemmann-like protein (PLML) SEQ ID NO:10.
PN US2005101558-A1.
PD 12-MAY-2005.
PA (WATT/) WATT A T.
Query Match 46.5%; Score 214.5; DB 9; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.3e-19;
RESULT 695
ID AEB29726 standard; protein; 87 AA.
DE Human FXD domain-containing ion transport regulator 3.
PN WO2005067667-A2.
PD 28-JUL-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 46.5%; Score 214.5; DB 9; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.3e-19;
RESULT 696
ID AED74451 standard; protein; 87 AA.
DE Human placental protein SEQ ID NO:1279.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match 46.5%; Score 214.5; DB 9; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.3e-19;
RESULT 697
ID ABJ19334 standard; protein; 116 AA.
DE NOVX related protein SEQ ID No 34.
PN WO200299062-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 46.5%; Score 214.5; DB 6; Length 116;
Best Local Similarity 54.5%; Pred. No. 1.1e-18;
RESULT 698
ID ADO41668 standard; protein; 116 AA.

Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 664
ID ADM37965 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 665
ID ADY77745 standard; protein; 89 AA.
DE Neoplastic disease detection protein PRO1069.
FN US200509102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 461; DB 9; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 666
ID AEA38515 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, #143.
FN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 9; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 667
ID AED50195 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2005163766-A1.
PD 28-JUL-2005.
Query Match 100.0%; Score 461; DB 9; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 668
ID AEF12576 standard; protein; 89 AA.
DE Human PRO1069 protein SEQ ID NO:50.
FN US2006008901-A1.
PD 12-JAN-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 10; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 669
ID AEF74265 standard; protein; 89 AA.
DE Human PRO1069 protein SEQ ID NO:50.
FN US2005260847-A1.
PD 24-NOV-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W L.
Query Match 100.0%; Score 461; DB 10; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 670
ID AAW92958 standard; protein; 89 AA.
DE Human zsig44 protein.
FN WO9905276-A1.
PD 04-FEB-1999.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 98.0%; Score 452; DB 2; Length 89;
Best Local Similarity 98.9%; Pred. No. 5.8e-49;
RESULT 671

ID AAM38770 standard; protein; 89 AA.
DE Human polypeptide SEQ ID NO 1915.
FN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 98.0%; Score 452; DB 4; Length 89;
Best Local Similarity 98.9%; Pred. No. 5.8e-49;
RESULT 672
ID ADK14984 standard; protein; 89 AA.
DE Urinary specific protein #90.
FN WO2003057839-A2.
PD 17-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 98.0%; Score 452; DB 7; Length 89;
Best Local Similarity 98.9%; Pred. No. 5.8e-49;
RESULT 673
ID AAM40556 standard; protein; 117 AA.
DE Human polypeptide SEQ ID NO 5487.
FN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 98.0%; Score 452; DB 4; Length 117;
Best Local Similarity 98.9%; Pred. No. 8.3e-49;
RESULT 674
ID ADP07847 standard; protein; 89 AA.
DE Human secreted protein, seq id 330.
FN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 97.0%; Score 447; DB 8; Length 89;
Best Local Similarity 97.8%; Pred. No. 2.5e-48;
RESULT 675
ID ADN38892 standard; protein; 186 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:210.
FN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 81.1%; Score 374; DB 7; Length 186;
Best Local Similarity 94.7%; Pred. No. 1.2e-38;
RESULT 676
ID ADN38894 standard; protein; 318 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:212.
FN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 81.1%; Score 374; DB 7; Length 318;
Best Local Similarity 94.7%; Pred. No. 2.3e-38;
RESULT 677
ID AAE05362 standard; protein; 88 AA.
DE Mouse channel inducing factor precursor (CHIF) protein.
FN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 60.0%; Score 276.5; DB 4; Length 88;
Best Local Similarity 66.7%; Pred. No. 1e-26;
RESULT 678
ID ABE72374 standard; protein; 88 AA.
DE Murine protein isolated from skin cells SEQ ID NO: 698.
FN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 60.0%; Score 276.5; DB 5; Length 88;
Best Local Similarity 66.7%; Pred. No. 1e-26;
RESULT 679
ID AAW92966 standard; protein; 87 AA.
DE Rat CHIF protein.
FN WO9905276-A1.
PD 04-FEB-1999.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 55.6%; Score 256.5; DB 2; Length 87;
Best Local Similarity 61.5%; Pred. No. 3.4e-24;
RESULT 680
ID AAR90991 standard; protein; 88 AA.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 646
ID ADH98932 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 647
ID ADI02162 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 648
ID ADH90701 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 649
ID ADJ54838 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 650
ID ADJ98576 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 651
ID ADJ98746 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 652
ID ADH78905 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 653
ID ADJ99139 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 654
ID ADJ99309 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 655
ID ADJ98927 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 656
ID ADH79075 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 657
ID ADX00935 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 658
ID ADK14456 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 659
ID ADJ64609 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 660
ID ADM31505 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 661
ID ADM36552 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 662
ID ADM40357 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 663
ID ADM80905 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 664
ID ADJ99309 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
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DE Human secreted/transmembrane protein PRO1069.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 628
ID ADH02207 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 629
ID ADG69211 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 630
ID ADG85996 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 631
ID ADH24932 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 632
ID ADH39549 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 633
ID ADH20041 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 634
ID ADH02547 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 635
ID ADG69041 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 636
ID ADH07644 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180850-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 637
ID ADG86166 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 638
ID ADH24762 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 639
ID ADH25810 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 640
ID ADH38376 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 641
ID ADH57215 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 642
ID ADH52203 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 643
ID ADH49569 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 644
ID ADH90531 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 645
ID ADI11267 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181683-A1.
PD 25-SEP-2003.

ID ADH33099 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 610
ID ADH39202 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 611
ID ADH26130 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US20031068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 612
ID ADH83942 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 613
ID ADH19508 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 614
ID ADH85486 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 615
ID ADH06280 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 616
ID ADH30110 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 617
ID ADH24422 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 618

ID ADH33099 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 619
ID ADG69551 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 620
ID ADH07814 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 621
ID ADG85826 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 622
ID ADH39372 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 623
ID ADH33564 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 624
ID ADH33904 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 625
ID ADH01114 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 626
ID ADG69721 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 627
ID ADH21001 standard; protein; 89 AA.

DE Novel human secreted and transmembrane protein PRO1069.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 591
ID ADI93734 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 592
ID ADC52188 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 593
ID ADE74337 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 594
ID ADE74949 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 595
ID ADF35388 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 596
ID ADG11638 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 597
ID ADF96162 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 598
ID ADG04433 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 599
ID ADG00593 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 600
ID ADH06620 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 601
ID ADH06450 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 602
ID ADG68871 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 603
ID ADH27761 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 604
ID ADH25102 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 605
ID ADH33734 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 606
ID ADG82849 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 607
ID ADH02377 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 608
ID ADH07984 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 8; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;


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Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 554
ID ADH98252 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 555
ID ADH98592 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 556
ID ADH98082 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 557
ID AD105070 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 558
ID AD103420 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 559
ID AD104815 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 560
ID ADH78269 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 561
ID AD119613 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 562
ID ADH90361 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 563
ID AD103080 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 564
ID ADH7929 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 565
ID ADH97912 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 566
ID AD101297 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 567
ID AD101992 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 568
ID AD103250 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 569
ID AD111437 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 570
ID AD102339 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 571
ID AD111777 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
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DE Human secreted and transmembrane protein PRO1069.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 536
ID ADH37965 standard; protein; 89 AA.
DE Human secreted and transmembrane protein PRO1069.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 537
ID ADH57385 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 538
ID ADH53527 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 539
ID ADH53697 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 540
ID ADH52033 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 541
ID ADH49888 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 542
ID ADI25398 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 543
ID ADH90191 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 544
ID ADI25568 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.

PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 545
ID ADH97742 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 546
ID ADI35443 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 547
ID ADI03590 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 548
ID ADI11947 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 549
ID ADH90021 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 550
ID ADH99935 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 551
ID ADH98422 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 552
ID ADI11097 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 553
ID ADI11607 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

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Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 517
ID ADF95229 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 518
ID ADG12365 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 519
ID ADH24082 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 520
ID ADH34108 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 521
ID ADH29941 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 522
ID ADH23912 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 523
ID ADH09025 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 524
ID ADG85316 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 525
ID ADH24592 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 526
ID ADH37448 standard; protein; 89 AA.
DE Human secreted and transmembrane protein PRO1069.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 527
ID ADH02037 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 528
ID ADH37618 standard; protein; 89 AA.
DE Human secreted and transmembrane protein PRO1069.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 529
ID ADG85656 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 530
ID ADH24252 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 531
ID ADH38546 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 532
ID ADG83667 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 533
ID ADH29475 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 534
ID ADH27591 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 535
ID ADH37788 standard; protein; 89 AA.
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PD 10-APR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 498
ID ADC81919 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 499
ID ADD07561 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 500
ID ADC82452 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 501
ID ADD05673 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 502
ID ADD08632 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003073030-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 503
ID ADD06881 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 504
ID ADC83128 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 505
ID ADD55235 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 506
ID ADD36054 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 507
ID ADD56193 standard; protein; 89 AA.
DE Human PRO polypeptide #75.

PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 508
ID ADD54631 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 509
ID ADE26785 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 510
ID ADE26252 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 511
ID ADF67189 standard; protein; 89 AA.
DE Human PRO1069 amino acid sequence SEQ ID NO:262.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 512
ID ADG01055 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 513
ID ADG08608 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 514
ID ADG02668 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 515
ID ADG01375 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 516
ID ADF95550 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 460
 ID ABM77035 standard; protein; 89 AA.
 DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
 PN US2003054464-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 461
 ID ABO28214 standard; protein; 89 AA.
 DE Human secreted/transmembrane protein (PRO) #100.
 PN US2003064459-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 462
 ID ABM22995 standard; protein; 89 AA.
 DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
 PN US2003068757-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 463
 ID ABM30315 standard; protein; 89 AA.
 DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
 PN US2003068723-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 464
 ID ABM21775 standard; protein; 89 AA.
 DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
 PN US2003068741-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 465
 ID ABM21470 standard; protein; 89 AA.
 DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
 PN US2003068744-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 466
 ID ABM15001 standard; protein; 89 AA.
 DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
 PN US2003068766-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 467
 ID ABO41076 standard; protein; 89 AA.
 DE Human secreted/transmembrane protein (PRO) #100.
 PN US2003068694-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 468
 ID ABO36806 standard; protein; 89 AA.
 DE Human secreted/transmembrane protein (PRO) #100.
 PN US2003068715-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;

RESULT 469
 ID ABO37416 standard; protein; 89 AA.
 DE Human secreted/transmembrane protein (PRO) #100.
 PN US2003068726-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 470
 ID ABM75206 standard; protein; 89 AA.
 DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
 PN US2003104544-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 471
 ID ABM33486 standard; protein; 89 AA.
 DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
 PN US2003096357-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 472
 ID ABO46241 standard; protein; 89 AA.
 DE Human PRO polypeptide #100.
 PN US2003049760-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 473
 ID ADA82635 standard; protein; 89 AA.
 DE Human secreted/transmembrane protein (PRO) #100.
 PN US2003049755-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 474
 ID ADB85623 standard; protein; 89 AA.
 DE Novel human secreted and transmembrane protein PRO1069.
 PN US2003049735-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 475
 ID ADB96270 standard; protein; 89 AA.
 DE Human PRO polypeptide #75.
 PN US2003054403-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 476
 ID ABM31840 standard; protein; 89 AA.
 DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
 PN US2003068680-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 477
 ID ABM31230 standard; protein; 89 AA.
 DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
 PN US2003068762-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 461; DB 7; Length 89;
 Best Local Similarity 100.0%; Pred. No. 4.2e-50;
 RESULT 478
 ID ADB85943 standard; protein; 89 AA.
 DE Human secreted/transmembrane protein (PRO) #100.

PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 441
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064450-A1.
ID ABM13171 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 442
ID AB031874 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 443
ID ABM14086 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068683-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 444
ID ABM08291 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 445
ID AB040161 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068681-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 446
ID ABM74596 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 447
ID ABM33791 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 448
ID ABM20250 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 449
ID AB048742 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 450
ID ABO22550 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 451
ID ABR72807 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036122-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 452
ID ABO15449 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 453
ID ABR85164 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040065-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 454
ID ABO15144 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044919-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 455
ID ABO17279 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040077-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 456
ID ABM17568 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003044928-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 457
ID ADA06551 standard; protein; 89 AA.
DE Human secreted/transmembrane PRO polypeptide #75.
PN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 458
ID ADA39244 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003059782-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 459
ID ABR85469 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
RESULT 460
ID ABR85469 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 7; Length 89;

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DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064444-A1.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 422
ID ABO29434 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 423
ID ABO31264 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 424
ID ABM14391 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 425
ID ABM09816 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 426
ID ABO38941 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 427
ID ABM34706 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 428
ID ABO51182 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 429
ID ABO04008 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 430
ID ABO10478 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003036151-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 431
ID ABO53180 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 432
ID ABR77721 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 433
ID ABR78931 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 434
ID ABO24025 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 435
ID ABR93789 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 436
ID ABM01832 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 437
ID ABM78255 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 438
ID ABR90044 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 439
ID ADA22385 standard; protein; 89 AA.
DE Human secreted/transmembrane polypeptide PRO1069.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 440
ID ABM27570 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
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Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 393
ID ABR86730 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040072-A1.
PD 27-FEB-2003.

Query Match

Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
BEST LOCAL SIMILARITY 100.0%; Pred. No. 4.2e-50;

Result 394

ID ABR86730 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040073-A1.
PD 27-FEB-2003.

Query Match

Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
BEST LOCAL SIMILARITY 100.0%; Pred. No. 4.2e-50;

Result 395

ID ABO21857 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054475-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
BEST LOCAL SIMILARITY 100.0%; Pred. No. 4.2e-50;

Result 396

ID ABO20027 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032124-A1.
PD 13-FEB-2003.

Query Match

Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
BEST LOCAL SIMILARITY 100.0%; Pred. No. 4.2e-50;

Result 397

ID ABO24330 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003064467-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
BEST LOCAL SIMILARITY 100.0%; Pred. No. 4.2e-50;

Result 398

ID ABR86079 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049759-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
BEST LOCAL SIMILARITY 100.0%; Pred. No. 4.2e-50;

Result 399

ID ABM10731 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064455-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
BEST LOCAL SIMILARITY 100.0%; Pred. No. 4.2e-50;

Result 400

ID ABW76730 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054465-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
BEST LOCAL SIMILARITY 100.0%; Pred. No. 4.2e-50;

Result 401

ID ABR89434 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073170-A1.
PD 17-APR-2003.

Query Match

Best Local Similarity 100.0%; Score 461; DB 7; Length 89;
BEST LOCAL SIMILARITY 100.0%; Pred. No. 4.2e-50;

Result 402

ID ABM12561 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073176-A1.

Query Match

RESULT 365
ID ABL11341 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
FN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 366
ID ABO32948 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
FN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 367
ID ABO30654 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
FN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 368
ID ABO30959 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
FN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 369
ID ABM27265 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
FN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 370
ID ABM30010 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
FN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 371
ID ABM05546 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
FN US2003068698-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 372
ID ABM15611 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
FN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 373
ID ABM08596 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
FN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 374
ID ABR88214 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
FN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 375
ID ABO38026 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
FN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 376
ID ABO45936 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
FN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 377
ID ABM66739 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
FN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 378
ID ADB20312 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
FN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 379
ID ABM19640 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
FN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 380
ID ABO49352 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
FN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 381
ID ABO49657 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
FN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 382
ID ADA78564 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
FN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 383
ID ABR88214 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
FN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 346
ID ABR19945 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 347
ID ABO46851 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 348
ID ABO47156 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 349
ID ADA83269 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 350
ID ABR71587 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 351
ID ABR72197 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 352
ID ABR98536 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 353
ID ABO06906 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 354
ID ABR84859 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 355
ID ABR73417 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 356
ID ABR76511 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US200304932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 357
ID ABR73112 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 358
ID ABM18178 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 359
ID ABO20637 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 360
ID ABO25380 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 361
ID ABO25685 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 362
ID ABR94094 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 363
ID ADA92824 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 364
ID ABR80001 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

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PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 327
ID AB051487 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 328
ID AB051792 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 329
ID AB050572 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 330
ID ABR79696 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 331
ID ABM16958 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 332
ID AB017990 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 333
ID AB020942 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 334
ID ABR96901 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 335
ID ADA38703 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 336
ID ABM12256 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 337
ID ABM16348 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 338
ID ABM24215 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 339
ID ABM14696 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 340
ID ABM04577 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 341
ID ABM06766 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 342
ID ABM09206 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 343
ID AB039246 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 344
ID ABM75511 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 345
ID ABM25435 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
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PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 308
ID ABO22722 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003027255-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 309
ID ABO231027 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 310
ID ABR92569 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 311
ID ABR81526 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 312
ID ABM77950 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 313
ID ABR89739 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 314
ID ABM26655 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 315
ID ABM13781 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 316
ID ABO28519 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 317

ID ABO30349 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 318
ID ABM07376 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 319
ID ABM03967 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 320
ID ABO37111 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 321
ID ABO41686 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 322
ID ABO35281 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 323
ID ABM25130 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 324
ID ABO47522 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 325
ID ABO47827 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 326
ID ABO48437 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.

PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 289
ID ABO21247 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 290
ID ABO22162 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054477-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 291
ID ADA20084 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003055222-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 292
ID ABO34191 standard; protein; 89 AA.
DE Human secreted/transmembrane polypeptide PRO 1069.
PN US2003060601-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 293
ID ABR96596 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054460-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 294
ID ADA94478 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 295
ID ABR85774 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049753-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 296
ID ABR99756 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049763-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 297
ID ABR99756 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 298
ID ABR99756 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 299
ID ABO29739 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068700-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 300
ID ABO29739 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068736-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 301
ID ABO29739 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068736-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 302
ID ABO38331 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068767-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 303
ID ABO45631 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003073182-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 304
ID ABR20555 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104557-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 305
ID ADA81471 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003092121-A1.
PD 15-MAY-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 306
ID ABO16669 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 307
ID ABO18295 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044920-A1.

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Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 270
ID ADA79744 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 271
ID ABR96291 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054458-A1.
PD 20-NAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 272
ID ABR96291 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054458-A1.
PD 20-NAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 273
ID ABR96384 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049758-A1.
PD 13-NAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 274
ID ABR86689 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049772-A1.
PD 13-NAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 275
ID ABR16653 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064448-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 276
ID ABR29705 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064456-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 277
ID ABO29129 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068693-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 278
ID ABR23910 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068735-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 279
ID ABO20332 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032125-A1.
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ID ABM23300 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068753-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 280
ID ABM22080 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068742-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 281
ID ABO37721 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068756-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 282
ID ABM28485 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 283
ID ABM28790 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 284
ID ABM66434 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068737-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 285
ID ABM75816 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104547-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 286
ID ABM34096 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003096359-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 287
ID ABM34401 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003100061-A1.
PD 29-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 288
ID ABO20332 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032125-A1.
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 251
ID ABO50267 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 252
ID ABU9261 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 253
ID ABO04313 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 254
ID ABO05943 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 255
ID ABM18483 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 256
ID ADA2789 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 257
ID ABR97511 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 258
ID ABR80611 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 259
ID ABM01222 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 260
ID ABR88824 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003096353-A1.
PD 22-MAY-2003.

DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 261
ID ABM13476 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 262
ID ABM20860 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 263
ID ABO41991 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 264
ID ABO42601 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 265
ID ABM10121 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 266
ID ABO38636 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 267
ID ABM32876 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 268
ID ABM32876 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 269
ID ABM74901 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003096353-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 269
ID ABM74901 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003096353-A1.
PD 22-MAY-2003.

RESULT 232
ID ABO52402 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 233
ID ADA11912 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 234
ID ABO231720 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 235
ID ADB17295 standard; protein; 89 AA.
DE Human transmembrane PRO polypeptide (SeqID 50).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 236
ID ADA17790 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 237
ID ABR97206 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 238
ID ABR86994 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 239
ID ABM11036 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 240
ID ABM28180 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 241
ID ABO32179 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 242
ID ABM15306 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 243
ID ABM06461 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 244
ID ABM04272 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 245
ID ABM22385 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 246
ID ABM07681 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 247
ID ABO40771 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 248
ID ABM35418 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 249
ID ABM33181 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 250
ID ABO52707 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003049773-A1.
PD 13-MAR-2003.

PN US2003082717-A1. Length 89;
PD 01-MAY-2003. Score 461; DB 6; Length 89;
Query Match 100.0%; Pred. No. 4.2e-50;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 204
ID AEM76121 standard; protein; 89 AA. Length 89;
DE Human secreted polypeptide PRO1069, SEQ ID NO:200. Score 461; DB 6; Length 89;
PN US2003104548-A1. Pred. No. 4.2e-50;
PD 05-JUN-2003. Score 461; DB 6; Length 89;
PA (GETH) GENENTECH INC. Pred. No. 4.2e-50;
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 205
ID ABM25740 standard; protein; 89 AA. Length 89;
DE Human secreted polypeptide PRO1069, SEQ ID NO:200. Score 461; DB 6; Length 89;
PN US2003104542-A1. Pred. No. 4.2e-50;
PD 05-JUN-2003. Score 461; DB 6; Length 89;
PA (GETH) GENENTECH INC. Pred. No. 4.2e-50;
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 206
ID ASM26045 standard; protein; 89 AA. Length 89;
DE Human secreted polypeptide PRO1069, SEQ ID NO:200. Score 461; DB 6; Length 89;
PN US2003104543-A1. Pred. No. 4.2e-50;
PD 05-JUN-2003. Score 461; DB 6; Length 89;
PA (GETH) GENENTECH INC. Pred. No. 4.2e-50;
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 207
ID ADA21459 standard; protein; 89 AA. Length 89;
DE Human secreted/transmembrane polypeptide PRO1069. Score 461; DB 6; Length 89;
PN US2003054404-A1. Pred. No. 4.2e-50;
PD 20-MAR-2003. Score 461; DB 6; Length 89;
PA (GETH) GENENTECH INC. Pred. No. 4.2e-50;
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 208
ID ABO03398 standard; protein; 89 AA. Length 89;
DE Human secreted/transmembrane protein (PRO) #100. Score 461; DB 6; Length 89;
PN US2003036127-A1. Pred. No. 4.2e-50;
PD 20-FEB-2003. Score 461; DB 6; Length 89;
PA (GETH) GENENTECH INC. Pred. No. 4.2e-50;
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 209
ID ABO02483 standard; protein; 89 AA. Length 89;
DE Human secreted/transmembrane protein (PRO) #100. Score 461; DB 6; Length 89;
PN US2003040061-A1. Pred. No. 4.2e-50;
PD 27-FEB-2003. Score 461; DB 6; Length 89;
PA (GETH) GENENTECH INC. Pred. No. 4.2e-50;
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 210
ID ABO44263 standard; protein; 89 AA. Length 89;
DE Human secreted/transmembrane polypeptide PRO 1069. Score 461; DB 6; Length 89;
PN US2003018172-A1. Pred. No. 4.2e-50;
PD 23-JAN-2003. Score 461; DB 6; Length 89;
PA (GETH) GENENTECH INC. Pred. No. 4.2e-50;
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 211
ID ABR90654 standard; protein; 89 AA. Length 89;
DE Human secreted polypeptide PRO1069, SEQ ID NO:200. Score 461; DB 6; Length 89;
PN US2003036130-A1. Pred. No. 4.2e-50;
PD 20-FEB-2003. Score 461; DB 6; Length 89;
PA (GETH) GENENTECH INC. Pred. No. 4.2e-50;
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 212
ID ABR73722 standard; protein; 89 AA. Length 89;
DE Human secreted polypeptide PRO1069, SEQ ID NO:200. Score 461; DB 6; Length 89;
PN US2003054468-A1. Pred. No. 4.2e-50;
PD 20-MAR-2003. Score 461; DB 6; Length 89;
PA (GETH) GENENTECH INC. Pred. No. 4.2e-50;
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 213
ID ABO16974 standard; protein; 89 AA. Length 89;
DE Human secreted/transmembrane protein (PRO) #100. Score 461; DB 6; Length 89;
PN US2003036130-A1. Pred. No. 4.2e-50;
PD 20-MAR-2003. Score 461; DB 6; Length 89;
PA (GETH) GENENTECH INC. Pred. No. 4.2e-50;
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

ID AEW03662 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068722-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

RESULT 186

ID AM35113 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073183-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

RESULT 187

ID ARM26350 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104549-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

RESULT 188

ID ABO48132 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003049749-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

RESULT 189

ID ABR92874 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064462-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

RESULT 190

ID ASO24635 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003065159-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

RESULT 191

ID ADA37773 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003008297-A1.
PD 09-JAN-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

RESULT 192

ID ABM11646 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003064447-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

RESULT 193

ID ABM02747 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073184-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

RESULT 194

ID ABM16043 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003073184-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;

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Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 157
ID ABO05638 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 158
ID ABR74027 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 159
ID ABR95619 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 160
ID ABR80916 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 161
ID ABR81221 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 162
ID ABM00917 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 163
ID ABR88519 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 164
ID ABM77340 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 165
ID ABO28824 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 166
ID ABO31569 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 167
ID ABM07986 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 168
ID ABO40466 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 169
ID ABO35891 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 170
ID ABO44030 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 171
ID ADA77952 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 172
ID ABM24825 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 173
ID ABO03093 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 174
ID ABR90349 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 175
ID ABM17263 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
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DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 138
ID ABR69757 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 139
ID ABU80134 standard; protein; 89 AA.
DE Human PRO protein #100.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 140
ID ABU82499 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 141
ID ABU92183 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 142
ID ABU93403 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 143
ID ABO09956 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 144
ID ABO09041 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 145
ID ABU96463 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 146
ID ABU10889 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 147
ID ABU10609 standard; protein; 89 AA.

DE Human secreted/transmembrane protein #100.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 148
ID ABU81641 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 149
ID ABU72133 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 150
ID ABU95618 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 151
ID ABU96827 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 152
ID ABR70672 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 153
ID ABO05023 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 154
ID ABO08431 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 155
ID ABU8580 standard; protein; 89 AA.
DE Human secreted and transmembrane polypeptide PRO1069.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 156
ID ABO34094 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;

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Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 117
ID ABU94691 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 118
ID ABO04618 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 119
ID ABR70367 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 120
ID ABU92352 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 121
ID ABU98532 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 122
ID ABR65931 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 123
ID ABR64648 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 124
ID ABU59417 standard; protein; 89 AA.
DE Novel human secreted or transmembrane protein PRO1129.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 125
ID ABU79573 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 126
ID ABU92964 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 127
ID ABU84667 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 128
ID ABU91143 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 129
ID ABU90236 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 130
ID ABO09651 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 131
ID ABO10923 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 132
ID ABR70977 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 133
ID ABU98287 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 134
ID ABU87585 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 135
ID ABU91453 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 136
ID ABU89292 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 461; DB 6; Length 89;
RESULT 137
ID ABU84667 standard; protein; 89 AA.
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Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 97
ID ABU85982 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2003022300-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 98
ID ABU82269 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2003036136-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 99
ID ABU87280 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
FN US2003036138-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 100
ID ABU83752 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
FN US2003032109-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 101
ID AB008126 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
FN US2003040066-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 102
ID ABU92500 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
FN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 103
ID ABU81837 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2003032104-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 104
ID ABU66001 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2003036157-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 105
ID ABU81170 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069.
FN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 106
ID ABR59830 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
FN US2003032120-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;

Query Match      100.0%; Pred. No. 4.2e-50;
RESULT 107
ID ABU94018 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2003036155-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 108
ID ABU99871 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2003022296-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 109
ID ABR66541 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
FN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 110
ID ABR90959 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
FN US2003040058-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 111
ID AB053285 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 112
ID ABU58974 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, #105.
FN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 113
ID ABU94386 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
FN US2003017540-A1.
PD 23-JAN-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 114
ID ABU79268 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
FN US2003032106-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 115
ID ABU86597 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
FN US2003032129-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 116
ID ABU86902 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
FN US2003032131-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
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PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 77
ID ABUS90984 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2003018468-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 78
ID ABR67870 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 79
ID ABR65258 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 80
ID ABR68480 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 81
ID ABR71892 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US200302135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 82
ID ABUS9268 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, #105.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 83
ID ABUS5372 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 84
ID ABUS9062 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 85
ID ABUS3142 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 86
ID ABUS4998 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032123-A1.
PD 13-FEB-2003.

Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 87
ID ABUS0546 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 88
ID ABUS4057 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 89
ID ABUS3708 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 90
ID AB025965 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 91
ID ABR64953 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 92
ID ABQ27305 standard; protein; 89 AA.
DE Human secreted/transmembrane polypeptide PRO1069.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 93
ID ABR68785 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 94
ID ABQ6601 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 95
ID ABR99146 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 96
ID ABUS7030 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003027280-A1.
PD 06-FEB-2003.
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PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 57
ID ABR66846 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 58
ID AB016059 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 59
ID AB013765 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US200304916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 60
ID ABU71530 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 61
ID ABU65668 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, SEQ ID 200.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 62
ID AB007516 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 63
ID AB003703 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 64
ID ABR67151 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 65
ID AB015754 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 66
ID ABU56035 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, PRO1069.
PN US2003022298-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 67
ID ABU72311 standard; protein; 89 AA.
DE Human PRO polypeptide #25.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 68
ID ABU65363 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 69
ID ABU95308 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 70
ID ABU71211 standard; protein; 89 AA.
DE Human PRO1069 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 71
ID ABQ07821 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 72
ID ABR70062 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 73
ID ABR69395 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 74
ID AB001536 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 75
ID ABU81338 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 76
ID ABR60135 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003032137-A1.
```

PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 37
ID ABUS90900 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 38
ID ABO33959 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 39
ID ABR99451 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 40
ID ABR98841 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 41
ID ABO16364 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 42
ID ABR92264 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 43
ID ABO18905 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 44
ID ABR78326 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003054474-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 45
ID ABU71976 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 46

ID ABUS062 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 47
ID ABO00201 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 48
ID ABO11533 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 49
ID ABO02178 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 50
ID ABUS8752 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 51
ID ABUS3447 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 52
ID ABO06248 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 53
ID ABR59284 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 54
ID ABO09346 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 55
ID ABO19210 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 56
ID ABO11228 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.

PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 17
ID ABU82805 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 18
ID ABU89926 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 19
ID ABR68175 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 20
ID ABU60552 standard; protein; 89 AA.
DE Human secreted/transmembrane protein, #105.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 21
ID ABU96228 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 22
ID ABU92659 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 23
ID AB008736 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 24
ID AB002788 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 25
ID ABR74942 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 26
ID ABR94704 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 27
ID ABU13934 standard; protein; 89 AA.
DE Human PRO1069 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 28
ID ABU85677 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 29
ID ABU98937 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 30
ID ABU98052 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 31
ID ABU91758 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 32
ID ABU89451 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 33
ID ABU86292 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 34
ID ABU67505 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 35
ID ABU80533 standard; protein; 89 AA.
DE Human PRO protein #100.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 36
ID ABU72519 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.

OM protein - protein search, using sw model
Run on: November 21, 2006, 19:47:43 ; Search time 201 Seconds.
(without alignments)
202.449 Million cell updates/sec

Title: US-10-063-557-50
Perfect score: 461
Sequence: 1 MERVTLALLLGLALEAN.....HSPVPEKAIPITPGSATTC 89
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : A_Geneseq 8:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAY66705	standard; protein; 89 AA.				
DE	Membrane-bound protein PRO1069.					
PN	WO9363088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 461;	DB 3;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 2						
ID	AAY87258	standard; protein; 89 AA.				
DE	Human signal peptide containing protein HSPP-35					
PN	WO200000610-A2.					
PD	06-JAN-2000.					
PA	(INCY-) INCYTE PHARM INC.					
Query Match	100.0%;	Score 461;	DB 3;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 3						
ID	RAY85679	standard; protein; 89 AA.				
DE	Human kidney disease associated protein SEQ ID 11.					
PN	WO200061622-A2.					
PD	19-OCT-2000.					
PA	(INCY-) INCYTE PHARM INC.					
Query Match	100.0%;	Score 461;	DB 3;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 4						
ID	AAU29123	standard; protein; 89 AA.				
DE	Human PRO polypeptide sequence #100.					
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 461;	DB 3;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 5						
ID	AAB87550	standard; protein; 89 AA.				
DE	Human PRO1069.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 461;	DB 4;	Length 89;		
Best Local Similarity	100.0%;	Pred. No. 4.2e-50;				
RESULT 6						
ID	AAB65228	standard; protein; 89 AA.				
DE	Human PRO1069 (UNQ526) protein sequence SEQ ID NO:262.					

PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 7
ID ABG95875 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 5; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 8
ID ABUS8499 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 9
ID ABU88047 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 10
ID ABU84362 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 11
ID ABR66236 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 12
ID ABR65626 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 13
ID ABUS9566 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 14
ID ABUS8043 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 15
ID ABUS9121 standard; protein; 89 AA.
DE Novel human secreted or transmembrane protein PRO1069.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
RESULT 16
ID ABUS2633 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.